

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 23, 2002, 12:16:05 : Search time 10 Seconds

(without alignments)  
38.720 Million cell updates/sec

Title: US-09-613-355D-3

Perfect score: 10

Sequence: 1 NLGEHPVCD5 10

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	60.0	373	1 YIA6_YEAST	P40556 saccharomyc
2	6	60.0	708	1 RAFA_ECOLI	P16551 escherichia
3	6	60.0	808	1 GC51_SCHPO	O14255 schizosacch
4	6	60.0	898	1 TOP1_SYNY3	P73810 synecocyst
5	5	50.0	31	1 DEF2_MESAU	P81466 mesocricetu
6	5	50.0	33	1 DEF4_MESAU	P81468 mesocricetu
7	5	50.0	114	1 E413_ADE02	P03240 human adeno
8	5	50.0	116	1 NGF_NAJAT	P21377 naja atra
9	5	50.0	116	1 NGF_NAJAT	P01140 naja naja
10	5	50.0	119	1 PTHV_CHICK	P15743 gallus gall
11	5	50.0	131	1 YJG4_YEAST	P47038 saccharomyc
12	5	50.0	146	1 MUCA_SALTY	P07376 salmonella
13	5	50.0	149	1 YC13_ARCFU	O29055 archaeoglob
14	5	50.0	152	1 SODC_NPVOP	O12933 orgyia pseu
15	5	50.0	183	1 UBXC_YEAST	P29340 saccharomyc
16	5	50.0	209	1 NUGM_DICDI	P22237 dictyosteli
17	5	50.0	261	1 TAM_MYCTU	O53698 mycobacteri
18	5	50.0	309	1 DHL2_LACCO	P14295 lactobacilli
19	5	50.0	347	1 GYRA_MVAXE	P27065 mycobacteri
20	5	50.0	427	1 BIMI_YEAST	P40013 saccharomyc
21	5	50.0	354	1 URE2_YEAST	P23202 saccharomyc
22	5	50.0	371	1 NTF6_TOBAC	O40531 nicotiana t
23	5	50.0	422	1 SPML_SCHPO	G92398 schizosacch
24	5	50.0	449	1 PIV2_ADEMI	P12539 mouse adeno
25	5	50.0	451	1 MURD_BACSU	O03522 bacillus su
26	5	50.0	491	1 NMT_CRYNE	P34809 cryptococcu
27	5	50.0	505	1 C712_SOLME	P37118 solanum mel
28	5	50.0	507	1 C714_SOLME	P37117 solanum mel
29	5	50.0	510	1 INOI_ORISA	O64437 oryza sativ
30	5	50.0	547	1 CD19_MOUSE	P25918 mus musculu
31	5	50.0	556	1 ASNS_SCHPO	P78753 schizosacch
32	5	50.0	556	1 YDPA_SCHPO	O14013 schizosacch
33	5	50.0	589	1 IFEB_ACSU	P23731 ascaris suu

34	5	50.0	613	1 ISPG_CHLPN	Q928h0 chlamydia p
35	5	50.0	676	1 QRL_COTJA	P23499 coturnix co
36	5	50.0	679	1 DNLJ_HAEIN	P43813 haemophilus
37	5	50.0	731	1 DNLJ_ZYMMO	P24719 zymomonas m
38	5	50.0	738	1 ECT2_MOUSE	Q07139 mus musculu
39	5	50.0	741	1 RN5A_HUMAN	Q05823 homo sapien
40	5	50.0	768	1 PARC_NEIGO	P43874 neisseria g
41	5	50.0	776	1 SM4F_RAT	Q92143 rattus norv
42	5	50.0	777	1 SM4F_MOUSE	Q92143 mus musculu
43	5	50.0	813	1 VGLH_HSVMD	P36336 marek's dis
44	5	50.0	839	1 TOP1_SYNE7	P34185 synecococc
45	5	50.0	883	1 ECT2_HUMAN	Q9H8v3 homo sapien

## ALIGNMENTS

RESULT 1  
YIA6\_YEAST STANDARD: PRT: 373 AA.  
AC P40556;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 01-FEB-1995 (Rel. 31, Last annotation update)  
DE Putative mitochondrial carrier YIL006W.  
GN YIL006W.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N A  
RC STRAIN=5288C / AB972;  
RA Barrett B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,  
RA Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A.,  
RA Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M.,  
RA Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,  
RA Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,  
RA Walsh S.V., Whitehead S.;  
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
CC inner membrane (Potential).  
CC -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
CC -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC -----  
CC EMBL: Z38113; CAA86245.1; -  
CC PIR: S48451; S48451.  
CC SGD: S0001268; YIL006W.  
CC InterPro: IPR001993; Mitoch\_carrier.  
CC Pfam: PF00153; mito\_carr; 3.  
CC PROSITE: PS00215; MITOCH\_CARRIER; 2.  
CC Hypothetical protein; Mitochondrion; Inner membrane; Repeat;  
CC Transmembrane; Transp.  
CC TRANSMEM 81 101 POTENTIAL.  
CC FT TRANSMEM 142 162 POTENTIAL.  
CC FT TRANSMEM 166 186 POTENTIAL.  
CC FT TRANSMEM 236 256 POTENTIAL.  
CC SQ SEQUENCE 373 AA; 41954 MW; 976C767C1D40E8DF CRC64;  
Query Match 60.0%; Score 6; DB 1; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.8;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NLGEHP 6  
| | | | |



RA Miyajima N., Hirose M., Sugita M., Sasamoto S., Kimura T.,  
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,  
RA Okumura S., Shimo S., Takeuchi C., Wada T., Watanabe A.,  
RA Yamada M., Yasuda M., Tabata S.,  
RT "Sequence analysis of the genome of the unicellular cyanobacterium  
RT Synechocystis sp. strain PC6803. II. Sequence determination of the  
RT entire genome and assignment of potential protein-coding regions.";  
RL DNA Res. 3:109-136(1996).  
CC -!- FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE  
CC CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER.  
CC -!- CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded  
CC DNA, followed by passage and rejoining.  
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).  
CC -!- MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA  
CC BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK. IN  
CC WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS  
CC AT ONE END OF THE ENZYME-SEVERED DNA STRAND.  
CC -!- SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE  
CC FAMILY.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC -----  
CC EMBL: D90909; BAA17864.1; -;  
CC HSSP: P06612; 1ECL.  
CC InterPro: IPR003601; DNATopI\_ATP\_bind.  
CC InterPro: IPR003602; DNATopI\_DNA\_bind.  
CC InterPro: IPR000380; Pro.topoisomerase.  
CC InterPro: IPR002936; Toprim.  
CC Pfam: PF01131; Topoisom\_bac; 1.  
CC Pfam: PF01751; Toprim; 1.  
CC PRINTS: PR00417; PRTPISMRASE1.  
CC SMART: SM00437; TOPIAC; 1.  
CC SMART: SM00436; TOPIRC; 1.  
CC SMART: SM00493; TOPRIM; 1.  
CC PROSITE: PS00396; TOPOISOMERASE\_I\_PROK; 1.  
KW Isomerase; Topoisomerase; DNA-binding; Complete proteome.  
FT ACT\_SITE 320 320 DNA\_CLEAVAGE (BY SIMILARITY).  
SQ SEQUENCE 898 AA; 99340 MW; 941666597398EB3 CRC64;  
  
Query Match 60.0%; Score 6; DB 1; Length 898;  
Best Local Similarity 100.0%; Pred. No. 7.4;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0.  
  
Qy 1 NLGHP 6  
Db 721 NLGHP 726  
  
RESULT 5  
DEF2\_MESAU STANDARD: PRT: 31 AA.  
AC P81466;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Neutrophil defensin 2 (HAMP-2).  
OS Mesocricetus auratus (Golden hamster).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
OC Mesocricetus.  
OX NCBI\_TaxID=10036;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=97045125; PubMed=8890190;  
RA Mak P., Wojcik K., Thogersen I.B., Dubin A.;  
RT "Isolation, antimicrobial activities, and primary structures of  
RT hamster neutrophil defensins.";  
RL Infect. Immun. 64:4444-4449(1996).  
CC -!- FUNCTION: BACTERICIDAL ACTIVITY, GREATER AGAINST GRAM-POSITIVE  
CC -!- BACTERIA. LOW ANTI-FUNGI ACTIVITY.  
CC -!- SIMILARITY: BELONGS TO THE FAMILY OF CATIONIC/STATIN/DEFENSIN  
CC PEPTIDES.  
CC -!- CAUTION: THE HAMP-2 COULD BE A PRODUCT OF PROTEOLYTIC N-TERMINAL  
CC AMINO ACID REMOVAL FROM HAMP-4.  
CC InterPro: IPR001271; Defensin.  
CC Pfam: PF00323; defensins; 1.  
CC SMART: SM00048; DEFSN; 1.  
CC PROSITE: PS00269; DEFENSIN; 1.  
CC Defensin; Antibiolic; Fungicide.  
KW DISULFID 3 31 BY SIMILARITY.  
FT DISULFID 5 20 BY SIMILARITY.  
FT DISULFID 10 30 BY SIMILARITY.  
SQ SEQUENCE 33 AA; 3821 MW; 23097FE7D474AD65 CRC64;  
  
Query Match 50.0%; Score 5; DB 1; Length 33;  
Best Local Similarity 100.0%; Pred. No. 8.4;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.  
  
Qy 6 PVCDs 10  
Db 8 PVCDs 12

RL Infect. Immun. 64:4444-4449(1996).  
CC -!- FUNCTION: BACTERICIDAL ACTIVITY, GREATER AGAINST GRAM-POSITIVE  
CC -!- BACTERIA. LOW ANTI-FUNGI ACTIVITY.  
CC -!- SIMILARITY: BELONGS TO THE FAMILY OF CATIONIC/STATIN/DEFENSIN  
CC PEPTIDES.  
CC -!- CAUTION: THE HAMP-2 COULD BE A PRODUCT OF PROTEOLYTIC N-TERMINAL  
CC AMINO ACID REMOVAL FROM HAMP-4.  
CC InterPro: IPR001271; Defensin.  
CC Pfam: PF00323; defensins; 1.  
CC SMART: SM00048; DEFSN; 1.  
CC PROSITE: PS00269; DEFENSIN; 1.  
CC Defensin; Antibiolic; Fungicide.  
KW DISULFID 1 29 BY SIMILARITY.  
FT DISULFID 3 18 BY SIMILARITY.  
FT DISULFID 8 28 BY SIMILARITY.  
SQ SEQUENCE 31 AA; 3621 MW; 3DE9E747D474AD34 CRC64;  
  
Query Match 50.0%; Score 5; DB 1; Length 31;  
Best Local Similarity 100.0%; Pred. No. 8;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.  
  
Qy 6 PVCDs 10  
Db 6 PVCDs 10

RESULT 6  
DEF4\_MESAU STANDARD: PRT: 33 AA.  
ID DEF4\_MESAU  
AC P81468;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Neutrophil defensin 4 (HAMP-4).  
OS Mesocricetus auratus (Golden hamster).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
OC Mesocricetus.  
OX NCBI\_TaxID=10036;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=97045125; PubMed=8890190;  
RA Mak P., Wojcik K., Thogersen I.B., Dubin A.;  
RT "Isolation, antimicrobial activities, and primary structures of  
RT hamster neutrophil defensins.";  
RL Infect. Immun. 64:4444-4449(1996).  
CC -!- FUNCTION: BACTERICIDAL ACTIVITY, GREATER AGAINST GRAM-POSITIVE  
CC -!- BACTERIA. LOW ANTI-FUNGI ACTIVITY.  
CC -!- SIMILARITY: BELONGS TO THE FAMILY OF CATIONIC/STATIN/DEFENSIN  
CC PEPTIDES.  
CC -!- CAUTION: THE HAMP-2 COULD BE A PRODUCT OF PROTEOLYTIC N-TERMINAL  
CC AMINO ACID REMOVAL FROM HAMP-4.  
CC InterPro: IPR001271; Defensin.  
CC Pfam: PF00323; defensins; 1.  
CC SMART: SM00048; DEFSN; 1.  
CC PROSITE: PS00269; DEFENSIN; 1.  
CC Defensin; Antibiolic; Fungicide.  
KW DISULFID 3 31 BY SIMILARITY.  
FT DISULFID 5 20 BY SIMILARITY.  
FT DISULFID 10 30 BY SIMILARITY.  
SQ SEQUENCE 33 AA; 3821 MW; 23097FE7D474AD65 CRC64;  
  
Query Match 50.0%; Score 5; DB 1; Length 33;  
Best Local Similarity 100.0%; Pred. No. 8.4;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.  
  
Qy 6 PVCDs 10  
Db 8 PVCDs 12

RESULT 7  
E413\_ADE02

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ID E413_ADE02 STANDARD: PRT: 114 AA.
AC P03240;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-APR-1990 (Rel. 14, Last annotation update)
DE Probable early E4 13 kDa protein.
OS Human adenovirus type 2.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=10515;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82059444; PubMed=6985482;
KA Herisse J., Rigolet M., Dupont de Dinechin S., Calibert F.;
RT "Nucleotide sequence of adenovirus 2 DNA fragment encoding for the
RT carboxylic region of the fiber protein and the entire E4 region.";
RL Nucleic Acids Res. 9:4021-4042(1981).
CC -! MISCELLANEOUS; THIS PROBABLE PROTEIN WAS ASSIGNED BY CORRELATING
CC EM DATA AND S1 DIGESTION STUDIES.
CC -----
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CC -----
CC EMBL: J01917; ; NOT_ANNOTATED_CDS.
DR PIR: A03806; Q4ADD2.
KW Early protein.
SQ SEQUENCE 114 AA, 13321 MW; 72FB72749D563457 CRC64;

Query Match 50.0%; Score 5; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVEDS 10
DB 10 PVEDS 14

RESULT 8
NGF_NAJAT STANDARD: PRT: 116 AA.
ID NGF_NAJAT
AC P21377;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Nerve growth factor (NGF).
OS Naja atra (Chinese cobra), and
OS Naja naja kaouthia (Monocled cobra) (Naja naja siamensis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Elapinae; Naja.
OX NCBI_TaxID=8656, 8649;
RN [1]
RP SEQUENCE.
RC SPECIES=N.n.atra; TISSUE=Venom;
RX MEDLINE=90147847; PubMed=2619756;
RA Oda T., Ohta M., Inoue S., Ikeda K., Furukawa S., Hayashi K.;
RT "Amino acid sequence of nerve growth factor purified from the venom
RT of the Formosan cobra Naja naja atra.";
RL Biochem. Int. 19:909-917(1989).
RN [2]
RP SEQUENCE.
RC SPECIES=N.n.kaouthia; TISSUE=Venom;
RX MEDLINE=91138755; PubMed=1995338;
PA Inoue S., Oda T., Koyama J., Ikeda K., Hayashi K.;
RT "Amino acid sequences of nerve growth factors derived from cobra
RT venoms.";
RL FEBS Lett. 279:38-40(1991).
CC -! FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
CC NEURONS IN THE BRAIN.
CC -! SUBUNIT: HOMODIMER.
CC -! SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
DR PIR: A01401; NGNXXI.
DR PIR: S13927; S13927.
DR HSP: P01139; 1BET.
DR InterPro: IPR002400; GF_cysknot.
DR IncerPro: IPR002072; NGF.

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CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
CC NEURONS IN THE BRAIN.
CC -! SUBUNIT: HOMODIMER.
CC -! SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
DR PIR: S13965; S13965.
DR HSP: P01139; 1BET.
DR InterPro: IPR002400; GF_cysknot.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF_1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PRODOM: PD002052; NGF_1.
DR SMART: SM00140; NGF_1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS00270; NGF_2; 1.
KW Growth factor
FT DISULFID 14 78 BY SIMILARITY.
FT DISULFID 56 106 BY SIMILARITY.
FT DISULFID 66 108 BY SIMILARITY.
FT SEQUENCE 116 AA; 13064 MW; DAB35421093F3B06 CRC64;
SQ
Query Match 50.0%; Score 5; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGEH 5
DB 7 NLGEH 11

RESULT 9
NGF_NAJNA STANDARD: PRT: 116 AA.
ID NGF_NAJNA
AC P01140;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Nerve growth factor (NGF).
OS Naja naja (Indian cobra).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Elapinae; Naja.
OX NCBI_TaxID=35670;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=91138755; PubMed=1995338;
RA Inoue S., Oda T., Koyama J., Ikeda K., Hayashi K.;
RT "Amino acid sequences of nerve growth factors derived from cobra
RT venoms.";
RL FEBS Lett. 279:38-40(1991).
RN [2]
RP PRELIMINARY SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=76114772; PubMed=1247508;
RA Hoque-Angeletti R.A., Frazier W.A., Jacobs J.W., Niall H.D.;
RA Bradshaw R.A.;
RT "Purification, characterization, and partial amino acid sequence of
RT nerve growth factor from cobra venom.";
RL Biochemistry 15:26-34(1976)
CC -! FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
CC NEURONS IN THE BRAIN.
CC -! SUBUNIT: HOMODIMER.
CC -! SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
DR PIR: A01401; NGNXXI.
DR PIR: S13927; S13927.
DR HSP: P01139; 1BET.
DR InterPro: IPR002400; GF_cysknot.
DR IncerPro: IPR002072; NGF.

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us-09-613-355d-3.rsp

Wed Oct 23 14:06:09 2002

DR Pfam: PF00243; NGF; 1.  
 DR PRINTS: PR00438; GFCYSKNOT.  
 DR PRODOM: PD00268; NGF.  
 DR PRODOM: PD002052; NGF; 1.  
 DR SMART: SM00140; NGF; 1.  
 DR PROSITE: PS00248; NGF\_1; 1.  
 DR PROSITE: PS00270; NGF\_2; 1.  
 KW Growth factor.  
 FT DISULFID 14 78 BY SIMILARITY.  
 FT DISULFID 56 106 BY SIMILARITY.  
 FT DISULFID 66 108 BY SIMILARITY.  
 SQ SEQUENCE 116 AA; 13022 MW; DAB346B1093E7E06 CRC64;  
 Query Match 50.0%; Score 5; DB 1; Length 116;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 NLGEH 5  
 DB 7 NLGEH 11

RESULT 10  
 PTHY\_CHICK  
 ID PTHY\_CHICK STANDARD; PRT; 119 AA.  
 AC P15743;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Parathyroid hormone precursor (PTH).  
 DE Gallus gallus (Chicken).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89219100; PubMed=2710135;  
 RA Russell J., Sherwood L.M.  
 RT "Nucleotide sequence of the DNA complementary to avian (chicken)  
 RT preproparathyroid hormone mRNA and the deduced sequence of the  
 RT hormone precursor.";  
 RL Mol. Endocrinol. 3:325-331(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89284968; PubMed=3251402;  
 RA Khosla S., Demay M., Pines M., Hurwitz S., Potts J.T. Jr.,  
 RA Kronenberg H.M.  
 RT "Nucleotide sequence of cloned cDNAs encoding chicken  
 RT preproparathyroid hormone.";  
 RL J. Bone Miner. Res. 3:689-698(1988).  
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISRUPTING THE SALTS IN  
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.  
 CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.  
 CC  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; M31604; AAA49093.1;  
 CC EMBL; M36522; AAB02866.1;  
 CC PIR; A34937; A34937.  
 CC HSP; P01270; 1HPV.  
 CC InterPro: IPR001415; Parathyroid.  
 CC InterPro: IPR003625; Parathyroid\_hormn\_sub.  
 CC Pfam: PF01379; Parathyroid; 1.  
 CC ProDom: PD010687; Parathyroid\_hormn\_sub; 1.  
 CC SMART: SM00087; PTH; 1.  
 CC PROSITE: PS00335; PARATHYROID; 1.

KW Hormone; Signal.  
 FT SIGNAL 1 25  
 FT PROPEP 26 31  
 FT CHAIN 32 112 PARATHYROID HORMONE.  
 SQ SEQUENCE 119 AA; 13943 MW; B309D8E772997F6F CRC64;  
 Query Match 50.0%; Score 5; DB 1; Length 119;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 NLGEH 5  
 DB 41 NLGEH 45

RESULT 11  
 YJG4\_YEAST  
 ID YJG4\_YEAST STANDARD; PRT; 131 AA.  
 AC P47038; 1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-FEB-1996 (Rel. 36, Last annotation update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Hypothetical 13.9 kDa protein in SMC3-MRPL8 intergenic region.  
 DE YJL064W OR J1120 OR HRC131.  
 GN Saccharomyces cerevisiae (Baker's yeast).  
 OS Saccharomycetes cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=S288C;  
 RX MEDLINE=95282514; PubMed=7762302;  
 RA Vandenbol M., Durand P., Dion C., Portetelle D., Hilger F.;  
 RT "Sequence of a 17.1 kb DNA fragment from chromosome X of  
 RT Saccharomyces cerevisiae includes the mitochondrial ribosomal protein  
 RT L8.";  
 RL Yeast 11:57-60(1995).  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; Z49340; CAA89356.1;  
 CC EMBL; Z34288; CAA84058.1;  
 CC SGD; S0003600; YJL064W.  
 KW Hypothetical protein.  
 SQ SEQUENCE 131 AA; 13854 MW; 736E72054593EF3 CRC64;  
 Query Match 50.0%; Score 5; DB 1; Length 131;  
 Best Local Similarity 100.0%; Pred. No. 24;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 NLGEH 5  
 DB 109 NLGEH 113

RESULT 12  
 MUCA\_SALTY  
 ID MUCA\_SALTY STANDARD; PRT; 146 AA.  
 AC P07376; P14302;  
 DT 01-APR-1988 (Rel. 07, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Muca protein (EC 3.4.21.-) [Contains: Muca protein].  
 DE GN MUCA.  
 OS Salmonella typhimurium, and  
 OS Escherichia coli.  
 OG Plasmid IncN PKM101, and Plasmid IncN R46.

[illegible]

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-----  
 CC -!- SIMILARITY: BELONGS TO THE CU-ZN SUPEROXIDE DISMUTASE FAMILY.  
 CC -----  
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 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: X65473; CAA46467.1; -  
 DR EMBL: Z72918; CAA97146.1; -  
 DR PIR: S29088; S29088  
 DR HSSP: P15731; LQCO  
 DR SGD: S0003365; PEX4.  
 DR InterPro: IPR000608; UBQ\_conjugat.  
 DR Pfam: PF00179; UO\_con: 1.  
 DR SMART: SM00212; UBC2; 1.  
 DR PROSITE: PS00183; UBIQUITIN\_CONJUGAT\_1; 1.  
 DR PROSITE: PS0127; UBIQUITIN\_CONJUGAT\_2; 1.  
 KW Ubiquitin conjugation; Ligase; Multigene family; Peroxisome.  
 FT BINDING 115 UBIQUITIN (BY SIMILARITY).  
 FT SEQUENCE 183 AA; 21118 MW; D4E438B689F76CAD CRC64;  
 SQ  
 Query Match 50.0%; Score 5; DB 1; Length 183;  
 Best Local Similarity 100.0%; Pred. No. 31;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 PVCD5 10  
 Db 144 PVCD5 148  
 Search completed: October 23, 2002, 12:19:52  
 Job time : 11 secs

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 CC -!- SIMILARITY: BELONGS TO THE CU-ZN SUPEROXIDE DISMUTASE FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC -----  
 DR EMBL: U75930; AAC59028.1; -  
 DR HSSP: P00441; 4SOD.  
 DR InterPro: IPR001424; SOD\_CU\_ZN.  
 DR Pfam: PF00080; sodd; 1.  
 DR PRINTS: PR00068; CUZNDISMUTASE.  
 DR PRODOM: PD000469; SOD\_CU\_ZN; 1.  
 DR PROSITE: PS00087; SOD\_CU\_ZN\_1; 1.  
 DR PROSITE: PS00332; SOD\_CU\_ZN\_2; 1.  
 KW Late protein; Oxidoreductase; Copper; Zinc.  
 FT METAL 43 43 COPPER (BY SIMILARITY).  
 FT METAL 45 45 COPPER (BY SIMILARITY).  
 FT METAL 60 60 COPPER AND ZINC (BY SIMILARITY).  
 FT METAL 68 68 ZINC (BY SIMILARITY).  
 FT METAL 77 77 ZINC (BY SIMILARITY).  
 FT METAL 80 80 ZINC (BY SIMILARITY).  
 FT METAL 118 118 COPPER (BY SIMILARITY).  
 FT DISULFID 54 144 BY SIMILARITY.  
 SQ SEQUENCE 152 AA; 15855 MW; 2B78743FFB47BB0 CRC64;  
 Query Match 50.0%; Score 5; DB 1; Length 152;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LGHPH 6  
 Db 126 LGHPH 130  
 RESULT 15  
 UBCX\_YEAST STANDARD; PRT: 183 AA.  
 AC P29340;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Ubiquitin-conjugating enzyme E2-21 kDa (EC 6.3.2.19)  
 DE (Ubiquitin-protein ligase) (Ubiquitin carrier protein) (Peroxin-4).  
 GN PEX4 OR PAS2 OR UBC10 OR YGR133W.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92396219; PubMed=1326082;  
 RA Wiebel F.F., Kunau W.-H.;  
 RT "The Pas2 protein essential for peroxisome biogenesis is related to  
 RT ubiquitin-conjugating enzymes.";  
 RL Nature 359:73-76(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA van Dyck L., Skala J., de Wergifosse P., Purnelle B., Talla E.,  
 RA Nawrocki A., del Bino S., Goffeau A.;  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: CATALYZES THE COVALENT ATTACHMENT OF UBIQUITIN TO  
 CC OTHER PROTEINS. ESSENTIAL FOR PEROXISOME BIOGENESIS.  
 CC -!- CATALYTIC ACTIVITY: ATP + ubiquitin + protein lysine -> AMP +  
 CC diphosphate + protein N-ubiquityllysine.  
 CC -!- PATHWAY: SECOND STEP IN UBIQUITIN CONJUGATION.  
 CC -!- SUBCELLULAR LOCATION: Peroxisomal.  
 CC -!- MISCELLANEOUS: A CYSTEINE RESIDUE IS REQUIRED FOR  
 CC UBIQUITIN-THIOLESTER FORMATION.  
 CC -!- SIMILARITY: BELONGS TO THE UBIQUITIN-CONJUGATING ENZYME FAMILY.

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OM protein - protein search, using sw model

Run on: October 23, 2002, 12:14:14 : Search time 13 Seconds  
(without alignments)  
18,789 Million cell updates/sec

Title: US-09-613-355D-3  
Perfect score: 10  
Sequence: 1 NLGHPVCDs 10

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 231628 seqs, 24425594 residues

Word size : 0

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents, AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	50.0	35	2	US-08-142-551B-51
2	5	50.0	120	4	US-09-660-552-31
3	5	50.0	146	4	US-09-660-552-29
4	5	50.0	344	1	US-08-446-919A-4
5	5	50.0	371	2	US-08-837-593-8
6	5	50.0	600	3	US-08-904-871-3
7	5	50.0	607	3	US-09-335-409-9
8	5	50.0	607	4	US-09-568-102-9
9	5	50.0	607	4	US-09-567-969-9
10	5	50.0	607	4	US-09-568-480-9
11	5	50.0	607	4	US-09-568-486-9
12	5	50.0	607	4	US-09-568-472-9
13	5	50.0	741	2	US-08-462-481-2
14	5	50.0	741	2	US-08-436-771-2
15	5	50.0	741	2	US-08-434-998-2
16	5	50.0	741	2	US-08-434-998-4
17	5	50.0	741	2	US-08-487-797-2
18	5	50.0	741	2	US-08-487-797-4
19	5	50.0	741	2	US-08-479-895-2
20	5	50.0	741	2	US-08-479-895-2
21	5	50.0	741	3	PCT-US95-02058-2
22	5	50.0	741	3	PCT-US95-02058-4
23	5	50.0	741	5	PCT-US95-02058-5
24	5	50.0	2273	4	US-09-426-998-5
25	5	50.0	4	40.0	US-08-802-981-209
26	4	40.0	5	3	US-08-802-981-207
27	4	40.0	7	3	US-08-802-981-207

Sequence 14, Appl  
Sequence 11, Appl  
Sequence 204, Appl  
Sequence 11, Appl  
Sequence 11, Appl  
Patent No. 5190919  
Patent No. 5190919  
Patent No. 5190919  
Sequence 22, Appl  
Patent No. 5190919  
Sequence 23, Appl  
Sequence 8, Appl  
Sequence 8, Appl  
Sequence 1, Appl  
Sequence 8, Appl  
Sequence 8, Appl  
Sequence 50, Appl  
Sequence 8, Appl

1 US-08-201-046A-14  
2 US-08-726-136-11  
3 US-08-802-981-204  
4 US-09-103-434-11  
5 US-09-687-594-11  
6 5190919-38  
7 5190919-40  
8 5190919-7  
9 5190919-7  
10 5190919-31  
11 US-08-201-046A-22  
12 US-08-201-046A-23  
13 US-08-036-555B-8  
14 US-08-469-569-8  
15 US-08-218-023-1  
16 US-08-249-322A-8  
17 US-08-469-526A-8  
18 US-08-480-190-50  
19 US-08-734-591A-8  
20 US-08-734-591A-8

ALIGNMENTS

RESULT 1  
US-08-142-551B-51  
Sequence 51, Application US/08142551B  
Patent No. 5814503  
GENERAL INFORMATION:  
APPLICANT: Oldenburg, Kevin R.  
APPLICANT: Selick, Harold E.  
TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND  
TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: 699 Prince Street  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: US  
ZIP: 22313  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/142,551B  
FILING DATE: 25-OCT-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/077,296  
FILING DATE: 14-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/838,219  
FILING DATE: 12-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/965,677  
FILING DATE: 22-OCT-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Swiss, Gerald F.  
REGISTRATION NUMBER: 30,113  
REFERENCE/DOCKET NUMBER: 000324-010  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 854-7400  
TELEFAX: (415) 854-8275  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Modified-site

## us-09-613-355d-3.ra1

Wed Oct 23 14:06:04 2002

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; LOCATION: 35
; OTHER INFORMATION: /note= "where "Xaa" is selected
; OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
; OTHER INFORMATION: amide, or the sequence of amino acids comprising
; OTHER INFORMATION: residues 35-84 of PTH."
US-08-142-551B-51
Query Match 50.0%; Score 5; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NLGEH 5
DB 10 NLGEH 14
RESULT 2
US-09-660-552-31
; Sequence 31, Application US/09660552
; Patent No. 633178
; GENERAL INFORMATION:
; APPLICANT: LIVNEH, Zvi
; APPLICANT: BACHER REUVEN, Nina
; APPLICANT: TOMER, Guy
; TITLE OF INVENTION: METHODS OF REPLICATING A DNA MOLECULE FOR REPAIR OF DNA
; TITLE OF INVENTION: LESION DAMAGE
; TITLE OF INVENTION: OR FOR MUTAGENESIS
; FILE REFERENCE: LIVNEH-1B
; CURRENT FILING DATE: 2000-09-12
; PRIOR FILING DATE: 2000-09-12
; PRIOR FILING DATE: 2000-07-27
; PRIOR FILING DATE: 2000-07-27
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant MuA'
US-09-660-552-31
Query Match 50.0%; Score 5; DB 4; Length 120;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 EHPVC 8
DB 114 EHPVC 118
RESULT 3
US-09-660-552-29
; Sequence 29, Application US/09660552
; Patent No. 633178
; GENERAL INFORMATION:
; APPLICANT: LIVNEH, Zvi
; APPLICANT: BACHER REUVEN, Nina
; APPLICANT: TOMER, Guy
; TITLE OF INVENTION: METHODS OF REPLICATING A DNA MOLECULE FOR REPAIR OF DNA
; TITLE OF INVENTION: LESION DAMAGE
; TITLE OF INVENTION: OR FOR MUTAGENESIS
; FILE REFERENCE: LIVNEH-1B
; CURRENT FILING DATE: 2000-09-12
; PRIOR FILING DATE: 2000-07-27
; PRIOR FILING DATE: 2000-07-27
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Conjugative plasmid
US-09-660-552-29
Query Match 50.0%; Score 5; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 EHPVC 8
DB 140 EHPVC 144
RESULT 4
US-08-446-919A-4
; Sequence 4, Application US/08446919A
; Patent No. 5736389
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: EB1 Gene Product Binds to APC
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hanner & Allegretti, Ltd.
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.
; ZIP: 20001-4597
; COMPUTER READABLE FORM
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,919A
; FILING DATE:
; CLASSIFICATION: 544
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.49255
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202.508.9100
; TELEFAX: 202.508.9299
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Saccharomyces cerevisiae
; IMMEDIATE SOURCE:
; CLONE: Yeo016p
US-08-446-919A-4
Query Match 50.0%; Score 5; DB 1; Length 344;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NLGEH 5
DB 292 NLGEH 296
RESULT 5
US-08-837-593-8
; Sequence 8, Application US/08837593
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Wed Oct 23 14:06:04 2002

; Patent No. 5977442  
; GENERAL INFORMATION:  
; APPLICANT: Klessig, Daniel F.  
; APPLICANT: Zhang Zhugun  
; TITLE OF INVENTION: "No. 5977442el Salicylic Acid Induced  
; TITLE OF INVENTION: Map Kinase and its Use for Enhanced Disease Resistance in Plant  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman,  
; ADDRESSEE: P.C.  
; STREET: 1601 Market Street, Suite 720  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: United States of America  
; ZIP: 19103-2307  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/837,593  
; FILING DATE: April 21, 1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/029,805  
; FILING DATE: October 25, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reed, Janet E.  
; REGISTRATION NUMBER: 36,252  
; REFERENCE/DOCKET NUMBER: Rutgers 97-0016  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 563-4100  
; TELEFAX: (215) 563-4044  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 371 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
; US-08-837-593-8

Query Match 50.0%; Score 5; DB 2; Length 371;  
Best Local Similarity 100.0%; Pred. No. 84;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVCDS 10  
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|  
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|  
|  
Db 334 PVCDS 338

RESULT 6  
US-08-904-871-3  
; Sequence 3, Application US/08904871  
; Patent No. 6046014  
; GENERAL INFORMATION:  
; APPLICANT: Lagarias, John C  
; APPLICANT: Murphy, John T  
; TITLE OF INVENTION: PHYTOFLUORS AS FLUORESCENT LABELS  
; FILE REFERENCE: 2500.134US0 UC OTT Lagarias Patent  
; CURRENT APPLICATION NUMBER: US/08/904,871  
; CURRENT FILING DATE: 1997-08-01  
; EARLIER APPLICATION NUMBER: 60/023,217  
; EARLIER FILING DATE: 1996-08-02  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3

; LENGTH: 600  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE: Description of Artificial Sequence:: Sequence  
; OTHER INFORMATION: alignment Fig. 6 Alphy  
; US-08-904-871-3

Query Match 50.0%; Score 5; DB 3; Length 600;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
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QY 3 GEHPV 7  
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|  
Db 118 GEHPV 122

RESULT 7  
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; Sequence 9, Application US/09335409  
; Patent No. 6121029  
; GENERAL INFORMATION:  
; APPLICANT: Schupp, Thomas  
; APPLICANT: Ligon, James  
; APPLICANT: Molnar, Istvan  
; APPLICANT: Zirkle, Ross  
; APPLICANT: Cyr, Devon  
; APPLICANT: Goerlach, Joern  
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILOXONES  
; FILE REFERENCE: 4-30582A  
; CURRENT APPLICATION NUMBER: US/09/335,409  
; CURRENT FILING DATE: 1999-06-17  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 607  
; TYPE: PRT  
; ORGANISM: Sorangium cellulosum  
; US-09-335-409-9

Query Match 50.0%; Score 5; DB 3; Length 607;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGEHP 6  
|  
|  
|  
|  
|  
Db 487 LGEHP 491

RESULT 8  
US-09-568-102-9  
; Sequence 9, Application US/09568102  
; Patent No. 6346404  
; GENERAL INFORMATION:  
; APPLICANT: Schupp, Thomas  
; APPLICANT: Ligon, James  
; APPLICANT: Molnar, Istvan  
; APPLICANT: Zirkle, Ross  
; APPLICANT: Cyr, Devon  
; APPLICANT: Goerlach, Joern  
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILOXONES  
; FILE REFERENCE: 4-30582A  
; CURRENT APPLICATION NUMBER: US/09/568,102  
; CURRENT FILING DATE: 2000-05-10  
; PRIOR APPLICATION NUMBER: 09/335,409  
; PRIOR FILING DATE: 1999-06-17  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 607  
; TYPE: PRT  
; ORGANISM: Sorangium cellulosum  
; US-09-568-102-9

us-09-613-355d-3.ra1

wed Oct 23 14:06:04 2002

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Query Match          50.0%; Score 5; DB 4; Length 607;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGEHP 6
Db 487 LGEHP 491

RESULT 9
US-09-567-969-9
; Sequence 9, Application US/09567969
; Patent No. 6355457
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/567,969
; CURRENT FILING DATE: 2000-05-10
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 607
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-567-969-9

Query Match          50.0%; Score 5; DB 4; Length 607;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGEHP 6
Db 487 LGEHP 491

RESULT 10
US-09-568-480-9
; Sequence 9, Application US/09568480
; Patent No. 6355458
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568,480
; CURRENT FILING DATE: 2000-05-10
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 607
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-568-480-9

Query Match          50.0%; Score 5; DB 4; Length 607;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGEHP 6
Db 487 LGEHP 491

RESULT 11
US-09-568-486-9
; Sequence 9, Application US/09568486
; Patent No. 6355459
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568,486
; CURRENT FILING DATE: 2000-05-10
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 607
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-568-486-9

Query Match          50.0%; Score 5; DB 4; Length 607;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGEHP 6
Db 487 LGEHP 491

RESULT 12
US-09-568-472-9
; Sequence 9, Application US/09568472
; Patent No. 6358719
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568,472
; CURRENT FILING DATE: 2000-05-10
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 607
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-568-472-9

Query Match          50.0%; Score 5; DB 4; Length 607;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGEHP 6
Db 487 LGEHP 491
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RESULT 13
US-08-462-481-2
; Sequence 2, Application US/08462481
; Patent No. 5840577
; GENERAL INFORMATION:
; APPLICANT: Silverman, Robert H.
; APPLICANT: Hassel, Bret A.
; APPLICANT: Zhou, Alvin
; TITLE OF INVENTION: Aulmal 2'-5A- Dependent pNases and
; TITLE OF INVENTION: Encoding Sequence Therefor
; Patent No. 5840577
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: Florida
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462.481
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028.086
; FILING DATE: 08-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: CL11363-13
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305/527/2498
; TELEFAX: 305/764/4996
; INFORMATION FOR SEQ ID NO. 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 741 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-462-481-2

Query Match 50.0%; Score 5; DB 2; Length 741;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLGEH 5
Db 668 NLGEH 672

RESULT 14
US-08-436-771-2
; Sequence 2, Application US/08436771
; Patent No. 5861300
; GENERAL INFORMATION:
; APPLICANT: Silverman, Robert H.
; APPLICANT: Sengupta, Dibyendu N.
; TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors,
; TITLE OF INVENTION: Cells and Methods
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell
; STREET: 200 E. Broward Boulevard
; CITY: Fort Lauderdale
; STATE: Florida
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,771
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/198,973
; FILING DATE: 18-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: CL11363-16
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305/527/2498

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; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,771
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/198,973
; FILING DATE: 18-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: CL11363-16
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305/527/2498
; TELEFAX: 305/764/4996
; INFORMATION FOR SEQ ID NO. 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 741 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-436-771-2

Query Match 50.0%; Score 5; DB 2; Length 741;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLGEH 5
Db 668 NLGEH 672

RESULT 15
US-08-436-771-4
; Sequence 4, Application US/08436771
; Patent No. 5861300
; GENERAL INFORMATION:
; APPLICANT: Silverman, Robert H.
; APPLICANT: Sengupta, Dibyendu N.
; TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors,
; TITLE OF INVENTION: Cells and Methods
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell
; STREET: 200 E. Broward Boulevard
; CITY: Fort Lauderdale
; STATE: Florida
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,771
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/198,973
; FILING DATE: 18-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: CL11363-16
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305/527/2498

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us-09-613-355d-3.ra1

Wed Oct 23 14:06:04 2002

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; TELEFAX: 305/764/4996
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 741 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-436-771-4
Query Match      50.0%; Score 5; DB 2; Length 741;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGEH 5
Db 668 NLGEH 672

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Search completed: October 23, 2002, 12:16:18  
Job time : 14 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 23, 2002, 12:18:20 : Search time 16 Seconds  
(without alignments)  
60.056 Million cell updates/sec

Title: US-09-613-355D-3  
Perfect score: 10  
Sequence: 1 NLGHPVCD5 10

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR\_71.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	60.0	373	2 S48451	probable membrane
2	6	60.0	414	2 E75636	hypothetical prote
3	6	60.0	708	1 A43717	alpha-galactosidas
4	6	60.0	808	2 T39059	probable mannosyl-
5	6	60.0	898	2 S74903	DNA topoisomerase
6	6	60.0	925	2 T16235	hypothetical prote
7	5	50.0	90	2 S12848	maturatin (piva2)
8	5	50.0	114	1 Q4ADD2	early E4 13K prote
9	5	50.0	116	1 NGJXI	nerve growth facto
10	5	50.0	116	2 A58566	nerve growth facto
11	5	50.0	116	2 C72549	hypothetical prote
12	5	50.0	119	2 A34937	parathyroid hormon
13	5	50.0	131	2 S50807	probable membrane
14	5	50.0	143	2 B84459	hypothetical prote
15	5	50.0	145	1 ZW5CAP	mucA protein - Esc
16	5	50.0	146	2 S06775	hypothetical prote
17	5	50.0	149	2 D69401	superoxide dismuta
18	5	50.0	152	2 T10298	beta C protein - p
19	5	50.0	154	2 P04655	hypothetical prote
20	5	50.0	168	2 S64830	hypothetical prote
21	5	50.0	172	2 B84008	ubiquitin--protein
22	5	50.0	179	2 S29088	conserved hypothet
23	5	50.0	183	2 D87567	hypothetical prote
24	5	50.0	203	2 S25617	NADH dehydrogenase
25	5	50.0	209	2 S12247	hypothetical prote
26	5	50.0	209	2 C84162	hypothetical prote
27	5	50.0	211	2 S48779	LI protein - human
28	5	50.0	224	2 T51072	hypothetical prote
29	5	50.0	238	2 T51072	hypothetical prote

30	5	50.0	239	2 F83366	conserved hypothet
31	5	50.0	242	2 C83631	probable carbonic
32	5	50.0	246	2 A59218	nerve growth facto
33	5	50.0	261	2 D70837	hypothetical prote
34	5	50.0	274	2 T32736	hypothetical prote
35	5	50.0	284	2 T36286	pyrroline-5-carbox
36	5	50.0	288	2 B84862	hypothetical prote
37	5	50.0	291	2 AF3264	4-hydroxybutyryl-C
38	5	50.0	297	2 T46414	hypothetical prote
39	5	50.0	301	2 A32814	flagellar filament
40	5	50.0	310	2 JQ0114	L-2-hydroxyisocapr
41	5	50.0	322	2 T32263	hypothetical prote
42	5	50.0	344	2 S50474	polymyrase - Berne
43	5	50.0	351	2 S11237	glutathione transf
44	5	50.0	354	2 A39609	hypothetical prote
45	5	50.0	355	2 C70194	hypothetical prote

ALIGNMENTS

RESULT 1  
S48451  
probable membrane protein Y11006w - yeast (Saccharomyces cerevisiae)  
C:Species: Saccharomyces cerevisiae  
C:Date: 02-Dec-1994 #sequence\_revision 02-Dec-1994 #text\_change 31-Mar-2000  
C:Accession: S48451  
R:Rowley, N.  
submitted to the EMBL Data Library, August 1994  
A:Reference number: S48442  
A:Accession: S48451  
A:Molecule type: DNA  
A:Residues: 1-373 <ROW>  
A:Cross-references: GB:247047; EMBL:Z38113; NID:9603997; PID:g763340; MIPS:Y11006w  
C:Genetics:  
A:Map position: 9L  
C:Superfamily: ADP-ATP carrier protein; ADP-ATP carrier protein repeat homology  
C:Keywords: duplication; mitochondrion; transmembrane protein  
F:74-167/Domain: ADP-ATP carrier protein repeat homology <ACP1>  
F:79-95/Domain: transmembrane #status predicted <TM1>  
F:173-264/Domain: ADP-ATP carrier protein repeat homology <ACP2>  
F:236-252/Domain: transmembrane #status predicted <TM2>  
F:275-365/Domain: ADP-ATP carrier protein repeat homology <ACP3>

Query Match 60.0%; Score 6; DB 2; Length 373;  
Best Local Similarity 100.0%; Pred. No. 8.2;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGHP 6  
|||  
DB 209 NLGHP 214

RESULT 2  
E75636  
hypothetical protein - Deinococcus radiodurans (strain R1)  
C:Species: Deinococcus radiodurans  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 31-Mar-2000  
C:Accession: E75636  
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999  
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A:Reference number: A75250; MUID:20036896  
A:Accession: E75636  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-414 <WHI>  
A:Cross-references: GB:AE001827; NID:96460959; PID:96460981; TIGR:DB

A:Map position: plasmid  
A:Genome: plasmid  
A:Note: plasmid Cpl

Query Match 60.0%; Score 6; DB 2; Length 414;  
Best Local Similarity 100.0%; Pred. No. 8.9;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGEHPV 7  
Db 301 LGEHPV 306

# RESULT 3

alpha-galactosidase (EC 3.2.1.22), raffinose-specific - Escherichia coli plasmid D1021  
C:Species: Escherichia coli  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A43717, B35160  
R:Aslanidis, C.; Schmid, K.; Schmitt, P.  
J. Bacteriol. 171, 6753-6763, 1989  
A:Title: Nucleotide sequences and operon structure of plasmid-borne genes mediating uptake  
A:Reference number: A43717; MUID:90078124  
A:Accession: A43717  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-708 <ASL>  
A:Cross-references: GB:M27273; NID:g147504; PIDN:AAA24497.1; PID:g147505  
R:Aslanidis, C.; Schmitt, R.  
J. Bacteriol. 172, 2178-2180, 1990  
A:Title: Regulatory elements of the raffinose operon: nucleotide sequences of operator and  
A:Reference number: A35160; MUID:90202743  
A:Accession: B35160  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-6 <AS2>  
A:Cross-references: GB:M29849; NID:g147508; PIDN:AAA24501.1; PID:g551828  
C:Genetics:  
A:Gene: rafa  
A:Genome: plasmid  
A:Complex: homotetramer  
C:Function:  
A:Description: catalyzes the hydrolysis of raffinose to galactose and sucrose  
C:Superfamily: raffinose-specific alpha-galactosidase  
C:Keywords: glycoprotein; glycosidase; hydrolase

Query Match 60.0%; Score 6; DB 1; Length 708;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGEHPV 7  
Db 430 LGEHPV 435

# RESULT 4

T39059  
probable mannosyl-oligosaccharide glucosidase (EC 3.2.1.106) - fission yeast (Schizosaccharomyces  
C:Species: Schizosaccharomyces pombe  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 20-Jun-2000  
C:Accession: T39059  
R:Oliver, K.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.  
submitted to the EMBL Data Library, August 1997  
A:Reference number: 221824  
A:Accession: T39059  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-808 <OLI>  
A:Cross-references: EMBL:298603; PIDN:CAR11295.1; GSPDB:GN00066; SPDB:SPAC6G10.09  
A:Experimental source: strain 972h-; cosmid c6G10  
C:Genetics:  
A:Gene: SPDB:SPAC6G10.09  
A:Map position: 1

A:Introns: 80/1  
C:Keywords: glycosidase; hydrolase

Query Match 60.0%; Score 6; DB 2; Length 898;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGEHPV 7  
Db 192 LGEHPV 197

# RESULT 5

DNA topoisomerase I - Synecocystis sp. (strain PCC 6803)  
N:Alternate names: protein sir2058  
C:Species: Synecocystis sp.  
A:Variety: PCC 6803  
C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 20-Jun-2000  
C:Accession: S74903  
R:Kaneko, T.; Sato, S.; Kutsai, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O.; K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas  
DNA Res. 3, 109-136, 1996  
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis  
S.  
A:Reference number: S74322; MUID:97061201  
A:Accession: S74903  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-898 <KAN>  
A:Cross-references: EMBL:U09009; GB:AB001339; NID:g1652844; PIDN:PA017864.1; PID:g165  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
C:Genetics:  
A:Gene: topA  
C:Superfamily: bacterial type I DNA topoisomerase

Query Match 60.0%; Score 6; DB 2; Length 898;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGEHP 6  
Db 721 NLGEHP 726

# RESULT 6

T16235  
hypothetical protein F32A5.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep 1999  
C:Accession: T16235  
R:Pauley, A.  
submitted to the EMBL Data Library, July 1995  
A:Description: The sequence of C. elegans cosmid F32A5.  
A:Reference number: Z18482  
A:Accession: T16235  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-925 <PAU>  
A:Cross-references: EMBL:U09864; NID:g069026; FID:g669027; PIDN:AA045560.1; GESP:F32A  
A:Experimental source: strain Bristol N2  
C:Genetics:  
A:Gene: GESP:F32A5.1  
A:Introns: 36/3; 142/1, 172/2, 263/3; 340/1, 621/1 565/2, 566/2, 572/2 812/1

Query Match 60.0%; Score 6; DB 2; Length 925;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GEHPVC 8  
Db 6 GEHPVC 11

A:Reference number: A01401; MUID:76114772

A:Accession: A01401  
A:Molecule type: p-protein  
A:Residues: 1-11, p, 13-14, B, 16, TBT, 20-21, GV, 23-27, N, 29-31, AS, 34, S, 36-48, 15-116 <HOG>  
A:Experimental source: venom  
A:Note: The source is designated as Naja naja and referred to as Indian cobra, so we  
C:Comment: Nerve growth factor is necessary for the development of embryonic sympathetic  
C:Complex: homodimer  
C:Superfamily: nerve growth factor beta chain  
C:Keywords: growth factor; homodimer; venom  
F:14-78,56-106,66-108/Disulfide bonds: \*status predicted

Query Match 50.0%; Score 5; DB 1; Length 116;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGEH 5  
Db 7 NLGEH 11

RESULT 10

A58566  
nerve growth factor - Chinese cobra  
C:Species: Naja naja atra (Chinese cobra)  
C:Date: 16-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 25-Apr-1997  
C:Accession: A58566  
R:Oda, T.; Ohta, M.; Inoue, S.; Ikeda, K.; Furukawa, S.; Hayashi, K.  
Biochem. Int. 19, 909-917, 1989  
A:Title: Amino acid sequence of nerve growth factor purified from the venom of the Fo  
A:Reference number: A58566; MUID:90147847  
A:Accession: A58566  
A:Molecule type: protein  
A:Residues: 1-116 <ODA>  
A:Experimental source: venom  
C:Comment: Nerve growth factor is necessary for the development of embryonic sympathetic  
C:Complex: homodimer  
C:Superfamily: nerve growth factor beta chain  
C:Keywords: growth factor; homodimer; venom  
F:14-78,56-106,66-108/Disulfide bonds: \*status predicted

Query Match 50.0%; Score 5; DB 2; Length 116;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGEH 5  
Db 7 NLGEH 11

RESULT 11

C72549  
hypothetical protein APE1679 - Aeropyrum pernix (strain K1)  
C:Species: Aeropyrum pernix  
C:Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Aug-1999  
C:Accession: C72549  
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Tawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.  
DNA Res. 6, 83-101, 1999  
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero  
A:Reference number: A72450; MUID:99310339  
A:Accession: C72549  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1116 <RAW>  
A:Cross-references: DDBJ:AP0000062; NID:95185244; PIDN:RAA0000001; PIP:J1044466; PID:q  
A:Experimental source: strain K1  
C:Genetics:  
A:Gene: APE1679

Query Match 50.0%; Score 5; DB 2; Length 116;  
Best Local Similarity 100.0%; Pred. No. 47;

RESULT 7

SI2848  
maturation (p1va2) protein - mouse adenovirus 1 (fragment)  
C:Species: Mastadenovirus mus1 (mouse adenovirus 1)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 30-Sep-1993  
C:Accession: SI2848  
R:King, S.C.; Spindler, K.R.  
Nucleic Acids Res. 18, 4003, 1990  
A:Title: Sequence of mouse adenovirus type 1 DNA encoding the amino terminus of protein  
A:Reference number: SI2848; MUID:90326539  
A:Accession: SI2848  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-90 <KRI>  
C:Superfamily: adenovirus maturation protein

Query Match 50.0%; Score 5; DB 2; Length 90;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGEH 5  
Db 18 NLGEH 22

RESULT 8

Q4ADD2  
early E4 13K protein - human adenovirus 2  
C:Species: Mastadenovirus h2 (human adenovirus 2)  
A:Note: host Homo sapiens (man)  
C:Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 04-Mar-1994  
R:Herisse, J.; Rigolet, M.; Dupont de Dinechin, S.; Galibert, F.  
Nucleic Acids Res. 9, 4023-4042, 1981  
A:Title: Nucleotide sequence of adenovirus 2 DNA fragment encoding for the carboxylic re  
A:Reference number: A93733; MUID:82059444  
A:Accession: A03806  
A:Molecule type: DNA  
A:Residues: 1-114 <HER>  
A:Note: this probable protein was assigned by correlating EM data and S1 digestion studi  
C:Genetics:  
A:Map position: 95.0-96.0  
C:Superfamily: adenovirus early E4 13K protein  
C:Keywords: early protein

Query Match 50.0%; Score 5; DB 1; Length 114;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVCDS 10  
Db 10 PVCDS 14

RESULT 9

NGNXXI  
nerve growth factor - Indian cobra  
C:Species: Naja naja naja (Indian cobra)  
C:Date: 30-Nov-1980 #sequence\_revision 25-Apr-1997 #text\_change 17-Mar-2000  
C:Accession: SI3927; A01401  
R:Inoue, S.; Oda, T.; Koyama, J.; Ikeda, K.; Hayashi, K.  
FEBS Lett. 279, 38-40, 1991  
A:Title: Amino acid sequences of nerve growth factors derived from cobra venoms.  
A:Reference number: SI3927; MUID:91138755  
A:Accession: SI3927  
A:Molecule type: protein  
A:Residues: 1-116 <INO>  
A:Experimental source: venom  
A:Note: the source is designated as Naja naja and referred to as Indian cobra, so we hav  
R:Hoque-Angeletti, R.A.; Frazier, W.A.; Jacobs, J.W.; Niall, H.D.; Bradshaw, R.A.  
Biochemistry 15, 26-34, 1976  
A:Title: Purification, characterization, and partial amino acid sequence of nerve growth

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GEPV 7  
|||||

Db 91 GEPV 95

RESULT 12

parathyroid hormone precursor chicken

C:Species: Gallus gallus (chicken)

C>Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 16-Jul-1999

C:Accession: A34937; I50411

R:Russell, J.; Sherwood, L.M. 1989

Mol. Endocrinol. 3, 325-331.

A:Title: Nucleotide sequence of the DNA complementary to avian (chicken) preproparathyroid hormone.

A:Reference number: A34937; MUID:89219100

A:Accession: A34937

A:Molecule type: mRNA

A:Residues: 1-119 <RUS>

A:Cross-references: GB:M31604; NID:q212767; PIDN:AAA49093.1; PID:q212768

R:Khosla, S.; Demay, M.; Pines, M.; Hurwitz, S.; Potts, J.T.

J. Bone Miner. Res. 3, 689-698, 1988

F:1-25/Domain: signal sequence #status predicted <SIG>

F:26-31/Domain: propeptide #status predicted <PRO>

F:30-64/Domain: parathyroid hormone homology <PTH>

F:32-119/Product: parathyroid hormone #status predicted <MAT>

A:Accession: I50411

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-119 <RUS>

A:Cross-references: GB:M36522; NID:q212591; PIDN:AA802865.1; PID:q212592

C:Superfamily: parathyroid hormone; parathyroid hormone homology

F:1-25/Domain: signal sequence #status predicted <SIG>

F:26-31/Domain: propeptide #status predicted <PRO>

F:30-64/Domain: parathyroid hormone homology <PTH>

F:32-119/Product: parathyroid hormone #status predicted <MAT>

Query Match 50.0%; Score 5; DB 2; Length 119;  
Best Local Similarity 100.0%; Pred. No. 48;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGEH 5  
|||||

Db 41 NLGEH 45

RESULT 13

S50807

probable membrane protein YJL064w - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein HRC131; hypothetical protein J1120

C:Species: Saccharomyces cerevisiae

C>Date: 13-Jan-1995 #sequence\_revision 08-Sep-1995 #text\_change 21-Jul-2000

C:Accession: S50807; S47126; S56838

R:Vandenbol, M.; Durand, P.; Dion, C.; Portetelle, D.; Hilger, F.

Yeast 11, 57-60, 1995

A:Title: Sequence of a 17.1 kb DNA fragment from chromosome X of Saccharomyces cerevisiae

A:Reference number: S50798; MUID:95282514

A:Accession: S50807

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-131 <VAN>

A:Cross-references: EMBL:Z34288; NID:g498992; PIDN:CAA84058.1; PID:g499002

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994

R:Vandenbol, M.; Durand, P.; Dion, C.; Portetelle, D.; Hilger, F.

submitted to the EMBL Data Library, June 1994

A:Description: Sequence analysis of a 17.1 kb DNA fragment from chromosome X of Saccharomyces cerevisiae

A:Reference number: S47126

A:Accession: S47126

A:Molecule type: DNA

A:Residues: 1-131 <VAN>

A:Cross-references: EMBL:Z34288; NID:g498992; PID:g499002

R:Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.

submitted to the Protein Sequence Database, September 1995

A:Reference number: S56835

A:Accession: S56838

A:Molecule type: DNA

A:Residues: 1-131 <POH>

A:Cross-references: EMBL:Z49340; NID:g1008412; PID:g1508214; MUID:YJL064w

C:Genetics:

A:Map position: 10L

C:Superfamily: Saccharomyces probable membrane protein YJL064w

C:Keywords: transmembrane protein

Query Match 50.0%; Score 5; DB 2; Length 131;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGEH 5  
|||||

Db 109 NLGEH 113

RESULT 14

B84459

hypothetical protein At2g04580 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001

C:Accession: B84459

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, M.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487

A:Accession: B84459

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-143 <STO>

A:Cross-references: GB:AE002093; NID:g4895106; PIDN:AA33755.1; GSPTB:GN00139

C:Genetics:

A:Gene: At2g04580

A:Map position: 2

Query Match 50.0%; Score 5; DB 2; Length 143;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 HPVCD 9  
|||||

Db 117 HPVCD 121

RESULT 15

ZWECAP

mucA protein - Escherichia coli plasmid pKM101

C:Species: Escherichia coli

C>Date: 28-Dec-1987 #sequence\_revision 31-Dec-1996 #text\_change 28-May-1999

C:Accession: D23157; JQ0451

R:Perry, K.L.; Elledge, S.J.; Mitchell, B.B.; Marsh, L.; Walker, G.C.

Proc. Natl. Acad. Sci. U.S.A. 82, 4331-4335, 1985

A:Title: umuDC and mucAB operons whose products are required for UV light- and chemie

A:Reference number: A23157; MUID:85242678

A:Accession: D23157

A:Molecule type: DNA

A:Residues: 1-145 <PEP>

A:Cross-references: GB:M13388; NID:g150798; PIDN:AAA9827.1; PID:g150744

R:Tanooka, H.

submitted to JIPID, May 1990

A:Reference number: JQ0451

A:Contents: muc364

A:Accession: JQ0451

A:Molecule type: DNA

A:Residues: 1-12,'R',13-145 <TAN>

C:Comment: This is one of the two proteins encoded by the mucAB operon, the plasmid-b

operon is controlled by recA and lexA proteins.

C:Genetics:

A:Gene: mucB

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A: Genome: plasmid  
 C: Superfamily: lexA repressor  
 C: Keywords: induced mutagenesis; SOS mutagenesis  
 Query Match 50.0%; Score 5; DB 1; Length 145;  
 Best Local Similarity 100.0%; Pred. No. 57;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 EHPVC 8  
 Db 139 EHPVC 143

Search completed. October 23, 2002, 12:20:50  
 Job time : 19 secs



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RESULT 2
US-08-793-624-19
; Sequence 19, Application US/08793624C
; Patent No. 6150093
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Moore, Patrick S.
; TITLE OF INVENTION: Unique Associated Kaposi's Sarcoma Virus Sequences And
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 45185-C-PCT-US/JPW
; CURRENT APPLICATION NUMBER: US/08/793,624C
; CURRENT FILING DATE: 1997-02-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-08-793-624-19

Query Match 67.8%; Score 40; DB 4; Length 404;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LGHPVCD 9
DB 225 LGSPVCD 232

RESULT 3
PCT-US95-10194-19
; Sequence 19, Application PC/TUS9510194
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University in the City of New York
; APPLICANT: City
; TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
; TITLE OF INVENTION: SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10194
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45185-C-PCT/JPW/NSC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 404 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-837-593-8

Query Match 62.7%; Score 37; DB 2; Length 371;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LGHPVCD 10
DB 330 INEEPVCDS 338

RESULT 4
US-08-837-593-8
; Sequence 8, Application US/08837593
; Patent No. 5977442
; GENERAL INFORMATION:
; APPLICANT: Klessig, Daniel F.
; APPLICANT: Zhang Zhuqun
; TITLE OF INVENTION: "NO. 5977442el Salicylic Acid Induced
; TITLE OF INVENTION: Map Kinase and its Use for Enhanced Disease Resistance in P
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman,
; ADDRESSEE: P.C.
; STREET: 1601 Market Street, Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: United States of America
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,593
; FILING DATE: April 21, 1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/029,805
; FILING DATE: October 25, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Janet E.
; REGISTRATION NUMBER: 36,252
; REFERENCE/DOCKET NUMBER: Rutgers 97-0016
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4100
; TELEFAX: (215) 563-4044
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-837-593-8

Query Match 62.7%; Score 37; DB 2; Length 371;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LGHPVCD 10
DB 330 INEEPVCDS 338

RESULT 5
US-09-214-214A-7
; Sequence 7, Application US/09214214A
; Patent No. 6211150
; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C.
; APPLICANT: Cheung, Ellen N.
; APPLICANT: Hershenson, Susan I.

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; APPLICANT: Young, John D.
; TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS
; FILE REFERENCE: A-411A US Revised073100
; CURRENT APPLICATION NUMBER: US/09/214,214A
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: PCT/US97/12609
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: US 08/684,353
; PRIOR FILING DATE: 1996-07-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Human
; US-09-214-214A-7

Query Match          59.3%; Score 35; DB 4; Length 117;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GEHPVCDS 10
DB 9 GEYSVCDS 16

RESULT 6
US-09-255-953-7
; Sequence 7, Application US/09255953
; Patent No. 6271364
; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C.
; APPLICANT: Cheung, Ellen Ngai Yin
; APPLICANT: Herhenson, Susan I.
; APPLICANT: Young, John D.
; TITLE OF INVENTION: ANALOGS OF NT-3 (As Amended)
; FILE REFERENCE: A-411B
; CURRENT APPLICATION NUMBER: US/09/255,953
; CURRENT FILING DATE: 1999-02-23
; EARLIER FILING DATE: 1996-07-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Analog of
; OTHER INFORMATION: human NT-3.
; US-09-255-953-7

Query Match          59.3%; Score 35; DB 4; Length 117;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GEHPVCDS 10
DB 9 GEYSVCDS 16

RESULT 7
US-09-214-214A-5
; Sequence 5, Application US/09214214A
; Patent No. 6211150
; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C.
; APPLICANT: Cheung, Ellen N.
; APPLICANT: Herhenson, Susan I.
; APPLICANT: Young, John D.
; TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS
; FILE REFERENCE: A-411A US Revised073100
; CURRENT APPLICATION NUMBER: US/09/214,214A

; APPLICANT: Young, John D.
; TITLE OF INVENTION: ANALOGS OF CATIONIC PROTEINS
; FILE REFERENCE: A-411A US Revised073100
; CURRENT APPLICATION NUMBER: US/09/214,214A
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: PCT/US97/12609
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: US 08/684,353
; PRIOR FILING DATE: 1996-07-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Human
; US-09-214-214A-5

Query Match          59.3%; Score 35; DB 4; Length 118;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GEHPVCDS 10
DB 10 GEYSVCDS 17

RESULT 8
US-09-255-953-5
; Sequence 5, Application US/09255953
; Patent No. 6271364
; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C.
; APPLICANT: Cheung, Ellen Ngai Yin
; APPLICANT: Herhenson, Susan I.
; APPLICANT: Young, John D.
; TITLE OF INVENTION: ANALOGS OF NT-3 (As Amended)
; FILE REFERENCE: A-411B
; CURRENT APPLICATION NUMBER: US/09/255,953
; CURRENT FILING DATE: 1999-02-23
; EARLIER FILING DATE: 1996-07-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Analog of
; OTHER INFORMATION: human NT-3.
; US-09-255-953-5

Query Match          59.3%; Score 35; DB 4; Length 118;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GEHPVCDS 10
DB 10 GEYSVCDS 17

RESULT 9
US-07-979-630-3
; Sequence 3, Application US/07979630
; Patent No. 5488099
; GENERAL INFORMATION:
; APPLICANT: Persson, et al.
; TITLE OF INVENTION: Multifunctional Neurotrophic Factors
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591
; COMPUTER READABLE FORM:

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; TELE# 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-440-049-2
;
Query Match          59.3%; Score 35; DB 1; Length 119;
Best Local Similarity 75.0%; Pred. No. 24;
Matches      6; Conservative    1; Mismatches    1; Indels
;
QY      3 GEHPVCDs 10
DB      9 GEYSVCDs 16
;
RESULT 11
US-08-340-131-3
; Sequence 3, Application US/08340131
; Patent No. 5770577
; GENERAL INFORMATION:
; APPLICANT: Kinstler, Olaf B
; TITLE OF INVENTION: DERIVATIVES OF BDNF AND NT-3
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Angen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,131
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Mazza, Richard J.
; REFERENCE/DOCKET NUMBER: A-298
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-340-131-3
;
Query Match          59.3%; Score 35; DB 1; Length 119;
Best Local Similarity 75.0%; Pred. No. 24;
Matches      6; Conservative    1; Mismatches    1; Indels
;
QY      3 GEHPVCDs 10
DB      9 GEYSVCDs 16
;
RESULT 12
US-08-441-513A-2
; Sequence 2, Application US/08441513A
; Patent No. 5981480
; GENERAL INFORMATION:
; APPLICANT: Urfer, Roman
; APPLICANT: Presta, Leonard G.
; APPLICANT: Winslow, John W.
; TITLE OF INVENTION: Pantropic Neurotrophic Factors
; NUMBER OF SEQUENCES: 20
;

```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441-513A
FILING DATE: 15-May-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/253937
FILING DATE: 03-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P090503
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-441-513A-2

Query Match 59.3%; Score 35; DB 2; Length 119;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 1; Indels 0;

QY 3 GEHPVCDS 10
DB 9 GEYSVCS 16

RESULT 13
US-08-970-865-5
Sequence 5, Application US/08970865
Patent No. 6005081
GENERAL INFORMATION:
APPLICANT: Louis E. Burton, Charles H. Schmelzer, Joanne T. Beck
TITLE OF INVENTION: Purification of NGF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/970,865
FILING DATE: 14-Nov-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030838
FILING DATE: 11/15/1996
PRIOR APPLICATION DATA: 60/047855
APPLICATION NUMBER: 5/29/1997
ATTORNEY/AGENT INFORMATION:
NAME: NEUNER, George W
REGISTRATION NUMBER: 26964
REFERENCE/DOCKET NUMBER: 12345
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TEXT: 200291 STPE UP
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-910-691-12

Query Match 59.3%; Score 35; DB 3; Length 119;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 1; Indels 1;

QY 3 GEHPVCDS 10
DB 9 GEYSVCS 16

RESULT 14
US-08-910-691-12
Sequence 12, Application US/08910691
Patent No. 6015552
GENERAL INFORMATION:
APPLICANT: WATANABE, Tatsuya
APPLICANT: YOSHITOMI, Sumie
APPLICANT: SASADA, Reiko
TITLE OF INVENTION: THERAPEUTIC AGENT FOR NEUTROPENIA
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESS: CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,691
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/074,969
FILING DATE: 19930604
ATTORNEY/AGENT INFORMATION:
NAME: NEUNER, George W
REGISTRATION NUMBER: 26964
REFERENCE/DOCKET NUMBER: 12345
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TEXT: 200291 STPE UP
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-910-691-12

Query Match 59.3%; Score 35; DB 3; Length 119;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 1; Indels 1;

QY 3 GEHPVCDS 10
DB 9 GEYSVCS 16

```

Wed Oct 23 14:06:13 2002

DB 9 GEYSVCDS 16  
||: ||||

RESULT 15  
US-08-581-662-2  
; Sequence 2, Application US/08581662  
; Patent No. 6121235  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Wei-Qiang  
; TITLE OF INVENTION: Treatment of Balance Impairments  
; FILE REFERENCE: P0981  
; CURRENT APPLICATION NUMBER: US/08/581,662  
; CURRENT FILING DATE: 1995-12-29  
; NUMBER OF SEQ ID NOS: 36  
; SEQ ID NO 2  
; LENGTH: 119  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-581-662-2

Query Match 59.3%; Score 35; DB 3; Length 119;  
Best Local Similarity 75.0%; Pred No. 24;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GEHPVCDS 10  
||: ||||  
DB 9 GEYSVCDS 16

Search completed: October 23, 2002, 12:11:31  
Job time : 14 secs

Wed Oct 23 14:06:10 2002

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 23, 2002, 12:16:25 : Search time 28 Seconds  
(without alignments)  
61.784 Million cell updates/sec

Title: US-09-613-355D-3  
Perfect score: 10  
Sequence: 1 NLGHPVCD5 10

Scoring table: 0.0170  
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 0

Total number of hits satisfying chosen parameters 562222

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

- SPTREMBL19:\*
- 1: sp\_archaea:\*
  - 2: sp\_bacteria:\*
  - 3: sp\_fungi:\*
  - 4: sp\_human:\*
  - 5: sp\_invertebrate:\*
  - 6: sp\_mammal:\*
  - 7: sp\_mhc:\*
  - 8: sp\_organelle:\*
  - 9: sp\_phase:\*
  - 10: sp\_plant:\*
  - 11: sp\_rodent:\*
  - 12: sp\_virus:\*
  - 13: sp\_vertebrate:\*
  - 14: sp\_unclassified:\*
  - 15: sp\_rvirus:\*
  - 16: sp\_bacteriap:\*
  - 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	70.0	894	Q9W4N9	Q9W4N9 drosophila
2	6	60.0	416	Q9RZHO	Q9RZHO deinococcus
3	6	60.0	596	Q19953	Q19953 caenorhabdi
4	5	50.0	87	Q78479	Q78479 human immun
5	5	50.0	116	Q91V99	Q91V99 human immun
6	5	50.0	116	Q9YBB8	Q9YBB8 aeropyrum p
7	5	50.0	119	Q9VU23	Q9VU23 drosophila
8	5	50.0	124	Q9V32	Q9V32 drosophila
9	5	50.0	143	Q9S105	Q9S105 arabidopsis
10	5	50.0	148	Q9IC93	Q9IC93 human papil
11	5	50.0	148	Q9IC92	Q9IC92 human papil
12	5	50.0	162	Q02476	Q02476 poa semilat
13	5	50.0	168	Q07914	Q07914 saccharomyc
14	5	50.0	172	Q91677	Q91677 pseudomonas
15	5	50.0	179	Q9K8Y6	Q9K8Y6 bacillus ha
16	5	50.0	181	Q9CSW9	Q9CSW9 mus musculus

17	5	50.0	198	3	Q9USB1	Q9USB1 schizosacch
18	5	50.0	203	16	Q9A591	Q9A591 caulobacter
19	5	50.0	207	10	Q50032	Q50032 nanochloro
20	5	50.0	211	17	Q9HSY7	Q9HSY7 halobacteri
21	5	50.0	224	12	Q81990	Q81990 human papil
22	5	50.0	237	2	Q9X6N2	Q9X6N2 streptomyce
23	5	50.0	237	5	Q9U8T0	Q9U8T0 hirtodrosop
24	5	50.0	239	16	Q911P0	Q911P0 pseudomonas
25	5	50.0	242	16	Q91730	Q91730 caenorhabdi
26	5	50.0	255	5	Q44730	Q44730 caenorhabdi
27	5	50.0	264	2	Q93U6	Q93U6 terrabacter
28	5	50.0	268	10	Q932E0	Q932E0 arabidopsis
29	5	50.0	270	5	Q9N8L9	Q9N8L9 trypanosoma
30	5	50.0	273	2	Q9EYL3	Q9EYL3 streptomyce
31	5	50.0	273	2	Q9F2E6	Q9F2E6 streptomyce
32	5	50.0	278	13	Q9DGN8	Q9DGN8 gallus gall
33	5	50.0	284	2	Q9X8G1	Q9X8G1 streptomyce
34	5	50.0	288	10	Q92W83	Q92W83 arabidopsis
35	5	50.0	290	2	Q9PQ80	Q9PQ80 buchnera ap
36	5	50.0	291	4	Q9H8V1	Q9H8V1 homo sapien
37	5	50.0	292	16	Q9G849	Q9G849 rhizobium 1
38	5	50.0	304	2	Q57075	Q57075 s intergen
39	5	50.0	322	5	Q17066	Q17066 caenorhabdi
40	5	50.0	322	2	Q9FE25	Q9FE25 micromonosop
41	5	50.0	326	2	Q9F660	Q9F660 lactobacilli
42	5	50.0	328	11	Q9D065	Q9D065 mus musculu
43	5	50.0	346	4	Q9CBE0	Q9CBE0 homo sapien
44	5	50.0	346	4	Q95717	Q95717 homo sapien
45	5	50.0	346	4	Q9P020	Q9P020 homo sapien

## ALIGNMENTS

### RESULT 1

Q9W4N9	PRELIMINARY;	PRT: 889 AA.
AC Q9W4N9		
ID Q9W4N9		
DT 01-MAY-2000 (TREMBlrel. 13, Created)		
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)		
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)		
DE CG2941 PROTEIN.		
GN CG2941.		
OS Drosophila melanogaster (Fruit fly).		
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC Ephydroidea; Drosophilidae; Drosophila.		
OX NCBI_TaxID=7227;		
[1]		
RN	SEQUENCE FROM N.A.	
RP		
RC STRAIN=BERKELEY;		
RX MEDLINE=20196006; PubMed=10731132;		
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,		
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,		
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,		
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,		
RA Brandon R.C., Rogers Y.-H.C., Blazer V., Champ M., Pfeiffer B.D.,		
RA Wan K.H., Doyle C., Baxter E.G., Helt J., Nelson C.R., Miklos G.L.G.,		
RA April J.F., Adayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,		
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,		
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,		
RA Borkova D., Botchan M.P., Bouck J., Brokstein P., Brotter P.,		
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,		
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,		
RA de Fabios B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,		
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,		
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieri S., Fleischmann W.,		
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,		
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,		
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.F., Houck J.,		
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,		
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,		
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,		

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RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merklov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders P.D.F., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Stadling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner P., Venier E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.:
RA "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL: AF003429; AAF45908.1; -
DR FlyBase: FBgn029686; CG2941.
SQ SEQUENCE 889 AA; 102407 MW; 7D9C8718E24813EC CRC64;

Query Match 70.0%; Score 7; DB 5; Length 889;
Best Local Similarity 100.0%; Pred. No. 0.92;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGHPVC 8
DB 309 LGHPVC 315
|||||

RESULT 2
Q9R2H0 PRELIMINARY: PRT; 414 AA.
AC Q9R2H0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE HYPOTHETICAL 45.0 KDA PROTEIN.
GN DR00015.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Mofat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
radiodurans R1.";
RL Science 286:1571-1577(1999).
DR EMBL: AE001827; AAF12684.1; -
DR TIGR: DR00015; -
DR InterPro: IPR002372; Bac_PQQ_repeat.
DR Pfam: PF01011; Bacterial_PQQ; 4.
KW Hypothetical protein; Plasmid; Complete proteome.
SQ SEQUENCE 414 AA; 45017 MW; 0859847AFD10D7D5 CRC64;

Query Match 60.0%; Score 6; DB 16; Length 414;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGHPV 7
DB 301 LGHPV 306
|||||

RESULT 3
Q19953 PRELIMINARY: PRT; 596 AA.
AC Q19953;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 70.0 KDA PROTEIN.
GN F32A5.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Phabditida; Phabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998)
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=BRISTOL N2;
RA Pauley A.;
RT "The sequence of C. elegans cosmid F32A5.";
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RP STRAIN=BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL EMBL: U20864; AAK68355.1; -
DR InterPro: IPR001005; Myb_DNA_bind.
DR InterPro: IPR000822; ZnF-C2H2.
DR Pfam: PF00249; myb_DNA-binding; 1.
DR SMART: SM00395; SANT; 1.
DR PROSITE: PS0090; MYB_3; 1.
DR PROSITE: PS00328; ZINC_FINGER_C2H2_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 596 AA; 69975 MW; 5626A6A81C0048F9 CRC64;

Query Match 60.0%; Score 6; DB 5; Length 596;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GEHPVC 8
DB 19 GEHPVC 24
|||||

RESULT 4
Q78479 PRELIMINARY: PRT; 87 AA.
AC Q78479;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE VIRAL SAMPLE IC33, V3 REGION (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92271245; PubMed=1589796;
RA Ou C.-Y., Gieselski C.A., Myers G., Bandea C.I., Luo C.C.,
RA Korber B.T.M., Mullins J.I., Schochetman G., Berkelman R.L.,
RA Economou A.N., Witte J.J., Furman L.J., Satten G.A., Curran J.W.,
RA Taffe H.W.;
RT "Molecular Epidemiology of HIV Transmission in a Dental Practice.";
RL Science 256:1165-1171(1992).

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DR EMBL: M90962; AAA44567.1; -.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
KW AIDS; Coat protein; Glycoprotein.  
FT NON\_TER 1  
FT NON\_TER 87  
FT NON\_TER 87  
SQ SEQUENCE 87 AA; 9657 MW; 8104141943CD4863 CRC64;  
  
Query Match 50.0%; Score 5; DB 15; Length 87;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 NLGEH 5  
Db 79 NLGEH 83  
  
RESULT 5  
Q91V99 PRELIMINARY; PRT: 116 AA.  
AC Q91V99;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 13, Last annotation update)  
DE REV PROTEIN.  
GN REV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
[1]  
RN SEQUENCE FROM N.A.  
RC STRAIN=V11035;  
RX MEDLINE=20418941; PubMed=10954895;  
RA Janssens W., Salminen M.O., Laukkanen T., Reyndrickx L.,  
Van der Auwera G., Colebunders R., McCutchan F.E., Van der Groen G.;  
"Near full-length genome analysis of HIV type 1 CRF02\_AG subtype C and  
RT CRF02\_AG subtype G recombinants";  
RL AIDS Res. Hum. Retroviruses 16:1183-1189(2000).  
DR EMBL: AJ276595; CAB82222.1; -.  
DR InterPro: IPR000625; REV.  
DR Pfam: PF00424; REV; 1.  
SQ SEQUENCE 116 AA; 12900 MW; 8147CE6b1655969B CRC64;  
  
Query Match 50.0%; Score 5; DB 15; Length 116;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 GEHPV 7  
Db 104 GEHPV 108  
  
RESULT 6  
Q9YBB8 PRELIMINARY; PRT: 116 AA.  
AC Q9YBB8;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE HYPOTHETICAL 12.4 KDA PROTEIN APE1679.  
GN APE1679.  
OS Aeropyrum pernix.  
OC Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;  
OX Aeropyrum.  
OX NCBI\_TaxID=56636;  
[1]  
RN SEQUENCE FROM N.A.  
RC STRAIN=K1;  
RX MEDLINE=99310339; PubMed=10382966;  
RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,  
Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,  
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,  
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,

RA Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,  
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;  
"Complete genome sequence of an aerobic hyper-thermophilic  
RT crenarchaeon, Aeropyrum pernix K1";  
RL DNA Res. 6:83-101(1999).  
DR EMBL: AP00062; BAA80680.1; -.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 116 AA; 12416 MW; 7400BD4327518C81 CRC64;  
  
Query Match 50.0%; Score 5; DB 17; Length 116;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 GEHPV 7  
Db 91 GEHPV 95  
  
RESULT 7  
Q9VUZ3 PRELIMINARY; PRT: 119 AA.  
AC Q9VUZ3;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)  
DE CG5157 PROTEIN.  
GN CG5157.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
[1]  
RN SEQUENCE FROM N.A.  
RC STRAIN=BERKELEY;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
RA George P.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.H.C., Blazer V.G., Champagne M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.P., Miklos G.L.G.,  
RA Abril J.F., Adayani A., An H.-J., Andrews-Trankoch C., Baldwin D.,  
RA Ballwey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Peinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
"The genome sequence of Drosophila melanogaster";

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RL Science 287:2185-2195(2000)
CC - SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL: AF003528; AAF49529.1; -.
DR HSSP: P04166; IAMP.
DR FlyBase: FBgn0036575; CG5157.
DR InterPro: IPR001199; Cyt_B5.
DR Pfam: PF00173; heme_1.
DR PRINTS: PR00363; CYTOCHROME_B5.
DR PROSITE: PS00191; CYTOCHROME_B5_1; UNKNOWN1.
DR PROSITE: PS00455; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 119 AA, 12622 MW, 2BACE178A5138BEF CRC64;

Query Match 50.0%; Score 5; DB 5; Length 119;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGEHP 6
DB 36 LGEHP 40

RESULT 8
Q9VY32 PRELIMINARY; PRT: 124 AA.
AC Q9VY32;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE CG14415 PROTEIN.
GN CG14415.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID:7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon P.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Beriman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington I., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos K., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun F.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

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RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Gibbs X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL: AF003495; AAF48373.1; -.
DR FlyBase: FBgn0030568; CG14415.
SQ SEQUENCE 124 AA, 13568 MW, E8139B765C943F57 CRC64;

Query Match 50.0%; Score 5; DB 5; Length 124;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGEHP 6
DB 22 LGEHP 26

RESULT 9
Q9SI05 PRELIMINARY; PRT: 143 AA.
AC Q9SI05;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PUTATIVE NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE
GN AT2G04580.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
OC Eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.B., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carreira A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana.";
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL, AC007231; AAD32755.1; -.
KW RNA-directed DNA polymerase.
SQ SEQUENCE 143 AA, 15900 MW, FCOEDFCC52F68FAD CRC64;

Query Match 50.0%; Score 5; DB 10; Length 143;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 HPVCD 9
DB 117 HPVCD 121

RESULT 10
Q91GY3 PRELIMINARY; PRT: 148 AA.
AC Q91GY3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MAJOR CAPSID PROTEIN (FRAGMENT).
GN L1.

```



OS Human papillomavirus.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OX NCBI\_TaxID=10566;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FA60.1;  
 RA Antonsson A., Hazard K., Hansson B.G.;  
 RT "Skin HPV found on foreheads."  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY040279; AAK74161.1; -  
 FT NON\_TER 1  
 FT NON\_TER 148  
 SQ SEQUENCE 148 AA; 16489 MW; DOA8961B564670C9 CRC64;

Query Match 50.0%; Score 5; DB 12; Length 148;  
 Best Local Similarity 100.0%; Pred. No. 62;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVCDS 10  
 Db 124 PVCDS 128

## RESULT 11

ID Q91GY2 PRELIMINARY; PRT; 148 AA.  
 AC Q91GY2;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE MAJOR CAPSID PROTEIN (FRAGMENT).  
 GN L1.  
 OS Human papillomavirus.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OX NCBI\_TaxID=10566;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FA60.2;  
 RA Antonsson A., Hazard K., Hansson B.G.;  
 RT "Skin HPV found on foreheads."  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY040280; AAK74162.1; -  
 FT NON\_TER 1  
 FT NON\_TER 148  
 SQ SEQUENCE 148 AA; 16517 MW; DOB977EB58A66DD4 CRC64;

Query Match 50.0%; Score 5; DB 12; Length 148;  
 Best Local Similarity 100.0%; Pred. No. 62;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVCDS 10  
 Db 124 PVCDS 128

## RESULT 12

ID Q02476 PRELIMINARY; PRT; 162 AA.  
 AC Q02476; Q85081;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
 DE BETA-C PROTEIN.  
 OS Poa semillatent virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hordeivirus.  
 OX NCBI\_TaxID=12328;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96204567; PubMed=8623558;  
 RA Solov'yev A.G., Savenkov E.I., Agranovsky A.A., Morozov S.Y.;  
 RT "Comparisons of the genomic cis-elements and coding regions in RNA

RT beta components of the hordeiviruses barley stripe mosaic virus.  
 RT lychmis ringspot virus, and poa semillatent virus."  
 RL Virology 219:9-18(1996).  
 RN [2]  
 RP SEQUENCE OF 9-162 FROM N.A.  
 RX MEDLINE=92356087; PubMed=1645144;  
 RA Agranovsky A.A., Karasev A.V., Novikov V.K., Lunina N.A., Loginov S.;  
 RA Tyulkina L.G.;  
 RT "Poa semillatent virus, a hordeivirus having no internal polydisperse  
 RT poly(A) in the 3' non-coding region of the RNA genome."  
 RL J. Gen. Virol. 73:2085-2092(1992).  
 DR EMBL: M81486; AAB05579.1; -  
 SQ SEQUENCE 162 AA; 18195 MW; 21EE3F104778261B CRC64;

Query Match 50.0%; Score 5; DB 12; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 67;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GEHPV 7  
 Db 105 GEHPV 109

## RESULT 13

ID Q07914 PRELIMINARY; PRT; 168 AA.  
 AC Q07914;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE CHROMOSOME XII PEAKING FRAME OFF YLR008C.  
 GN YLR008C.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Vandenbol M., Portetelle D., Hilger F.;  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MIPS;  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: Z73180; CAA97530.1; -  
 DR SGD: S0003995; YLR008C.  
 DR InterPro: IPR001623; DnaJ\_N.  
 DR Pfam: PF00226; DnaJ; 1.  
 DR SMART: SM00271; DnaJ; 1.  
 DR PROSITE: PS00076; DnaJ\_2; 1.  
 SQ SEQUENCE 168 AA; 17910 MW; 9CBF71CA50A0F341 CRC64;

Query Match 50.0%; Score 5; DB 3; Length 168;  
 Best Local Similarity 100.0%; Pred. No. 69;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GEHPV 7  
 Db 62 GEHPV 66

## RESULT 14

ID Q916Y7 PRELIMINARY; PRT; 172 AA.  
 AC Q916Y7;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)  
 DE HYPOTHETICAL PROTEIN PA0145.  
 GN PA0145.  
 OS Pseudomonas aeruginosa.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
 OC Pseudomonas.

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OX NCBI_TaxID=287;
RN {}
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RA "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; AE004452; AAG03535.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 172 AA: 18448 MW: 47F0EF465D6C51C9 CRC64;

Query Match 50.0%; Score 5; DB 16; Length 172;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGEHP 6
DB 122 LGEHP 126

RESULT 15
Q9K8Y6 PRELIMINARY: PRT: 179 AA.
AC Q9K8Y6;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE BH2866 PROTEIN.
GN BH2866.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=86665;
RN {}
RP SEQUENCE FROM N.A.
RC STRAIN-C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hiram C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RA "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AP001516; BA06585.1; -.
DR InterPro; IPR002819; HD.
DR InterPro; IPR003607; HDC.
DR Pfam; PF01966; HD: 1.
DR SMART; SM00471; HDC: 1.
KW Complete proteome.
SQ SEQUENCE 179 AA: 20576 MW: 4182BD2CFFACAC9F CRC64;

Query Match 50.0%; Score 5; DB 16; Length 179;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGEHP 6
DB 94 LGEHP 98

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Search completed. October 23, 2002, 12:20:28  
Job time : 31 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 23, 2002, 12:11:34 : Search time 25 Seconds  
(without alignments)  
69.198 Million cell updates/sec

Title: US-09-613-355d-3  
Perfect score: 59  
Sequence: 1 NLGHPVCD5 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_19:  
1: sp\_archaea:  
2: sp\_bacteria:  
3: sp\_fungi:  
4: sp\_human:  
5: sp\_invertebrate:  
6: sp\_mammal:  
7: sp\_mhc:  
8: sp\_organelle:  
9: sp\_phage:  
10: sp\_plant:  
11: sp\_rodent:  
12: sp\_virus:  
13: sp\_vertebrate:  
14: sp\_unclassified:  
15: sp\_rvirus:  
16: sp\_bacteriaph:  
17: sp\_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	72.9	889	5 Q9W4N9	Q9W4N9 drosophila
2	41	69.5	148	12 Q91GY3	Q91GY3 human papil
3	41	69.5	148	12 Q91GY2	Q91GY2 human papil
4	41	69.5	224	12 Q81990	Q81990 human papil
5	40	67.8	404	12 Q98141	Q98141 kaposi's sa
6	39	66.1	241	13 Q90W38	Q90W38 bothrops ja
7	39	66.1	324	13 Q9XY95	Q9XY95 lampetra fl
8	39	66.1	479	11 Q9D468	Q9D468 mus musculu
9	39	66.1	596	5 Q19953	Q19953 caenorhabdi
10	39	66.1	5170	5 Q17490	Q17490 caenorhabdi
11	39	66.1	6994	5 Q17343	Q17343 caenorhabdi
12	38	64.4	186	16 Q9JUF2	Q9JUF2 neisseria m
13	38	64.4	253	16 Q9JUF26	Q9JUF26 neisseria m
14	38	64.4	544	5 Q19339	Q19339 caenorhabdi
15	38	64.4	1529	3 Q9Y7C6	Q9Y7C6 aspergillus
16	37	62.7	108	13 Q98T10	Q98T10 anguilla an

17	37	62.7	116	13 Q98TH9	Q98TH9 anquilla an
18	37	62.7	371	10 Q9AYN8	Q9AYN8 nicotiana t
19	37	62.7	664	2 Q9RKL3	Q9RKL3 streptomyce
20	36	61.0	97	1 P70723	P70723 acidianus a
21	36	61.0	342	12 Q65844	Q65844 beet wester
22	36	61.0	395	2 Q69347	Q69347 vibrio sp.
23	36	61.0	454	10 Q40922	Q40922 pseudotsuga
24	36	61.0	676	10 Q4MUN5	Q4MUN5 arabidopsis
25	36	61.0	705	10 Q9SV85	Q9SV85 arabidopsis
26	36	61.0	734	10 Q9LN20	Q9LN20 arabidopsis
27	36	61.0	1037	4 Q9BX69	Q9BX69 homo sapien
28	36	61.0	1453	10 Q9AKV0	Q9AKV0 arabidopsis
29	36	61.0	1529	10 Q81068	Q81068 arabidopsis
30	35.5	60.2	359	4 Q96S59	Q96S59 homo sapien
31	35	59.3	79	13 Q9W7K1	Q9W7K1 pseudonaja
32	35	59.3	129	13 Q9W7K0	Q9W7K0 pseudonaja
33	35	59.3	129	11 Q9WU16	Q9WU16 mesocricetu
34	35	59.3	146	12 Q9WGF4	Q9WGF4 human papil
35	35	59.3	210	10 Q9PM00	Q9PM00 arabidopsis
36	35	59.3	241	6 Q9N182	Q9N182 macaca fusc
37	35	59.3	241	13 Q9DE29	Q9DE29 crocalus du
38	35	59.3	282	2 Q9S4F4	Q9S4F4 leptospira
39	35	59.3	286	13 Q91988	Q91988 xiphophorus
40	35	59.3	294	11 Q91XB4	Q91XB4 mus musculu
41	35	59.3	363	16 Q9PBW0	Q9PBW0 xylella fas
42	35	59.3	382	5 Q01933	Q01933 caenorhabdi
43	35	59.3	388	12 Q41927	Q41927 mutid hetige
44	35	59.3	422	10 Q9FKH8	Q9FKH8 arabidopsis
45	35	59.3	508	16 Q9Z878	Q9Z878 chlamydia p

#### ALIGNMENTS

#### RESULT 1

Q9W4N9 ID Q9W4N9 PRELIMINARY; PRT; 889 AA.  
AC Q9W4N9  
DT 01-MAY-2000 (TrEMBLrel 13, Created)  
DT 01-MAY-2000 (TrEMBLrel 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel 13, Last annotation update)  
DE CG2941 PROTEIN.  
GN CG2941.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BERKELEY;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,  
RA George F.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Dewle C., Baxter E.G., Holt G., Nelson C.P., Miklos G.L.G.,  
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Besley E.M.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harkin N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

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RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., M.G.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs P.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RT "The genome sequence of Drosophila melanogaster."  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AE003429; AAF45908.1; -;  
 DR FlyBase; FBgn0029686; CG2941.  
 SQ SEQUENCE 889 AA; 102407 MW; 7D9C8718E24813EC CRC64;

Query Match 72.9%; Score 43; DB 5; Length 889;  
 Best Local Similarity 100.0%; Pred. No. 7.3;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGHPVC 8  
 DB 309 LGHPVC 315  
 DB 116 LGHPVC 315

RESULT 2  
 Q91GY3 PRELIMINARY; PRT; 148 AA.  
 AC Q91GY3;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE MAJOR CAPSID PROTEIN (FRAGMENT).  
 GN L1.  
 OS Human papillomavirus.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OC NCBI\_TaxID=10566;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-FA60.1;  
 RA Antonsson A., Hazard K., Hansson B.G.,  
 RT "Skin HPV found on foreheads."  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY040279; AAK74161.1; -;  
 FT NON\_TER 1  
 FT NON\_TER 148  
 SQ SEQUENCE 148 AA; 16489 MW; D0A8961B564670C9 CRC64;

Query Match 69.5%; Score 41; DB 12; Length 148;  
 Best Local Similarity 69.2%; Pred. No. 2.8;  
 Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 2 LGHPVC 8  
 DB 116 LGHPVC 315  
 DB 116 LGHPVC 315

RESULT 3  
 Q91GY2 PRELIMINARY; PRT; 148 AA.  
 AC Q91GY2;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE MAJOR CAPSID PROTEIN (FRAGMENT).  
 GN L1.  
 OS Human papillomavirus.

Query Match 69.5%; Score 41; DB 12; Length 148;  
 Best Local Similarity 69.2%; Pred. No. 2.8;  
 Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 2 LGHPVC 8  
 DB 116 LGHPVC 315  
 DB 116 LGHPVC 315

RESULT 5  
 Q98141 PRELIMINARY; PRT; 404 AA.  
 ID Q98141;  
 AC Q98141; O12570;  
 DT 01-FEB-1997 (TREMBlrel. 02, Created)  
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
 DE ORF 23.  
 OS Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OC NCBI\_TaxID=10566;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-FA60.2;  
 RA Antonsson A., Hazard K., Hansson B.G.,  
 RT "Skin HPV found on foreheads."  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY040280; AAK74162.1; -;  
 FT NON\_TER 1  
 FT NON\_TER 148  
 SQ SEQUENCE 148 AA; 16517 MW; D0B977EB58A66D04 CRC64;

Query Match 69.5%; Score 41; DB 12; Length 148;  
 Best Local Similarity 69.2%; Pred. No. 2.8;  
 Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 2 LGHPVC 8  
 DB 116 LGHPVC 315  
 DB 116 LGHPVC 315

RESULT 4  
 Q81990 PRELIMINARY; PRT; 224 AA.  
 ID Q81990;  
 AC Q81990;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE CAPSID PROTEIN L1 (FRAGMENT).  
 GN L1.  
 OS Human papillomavirus.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OC NCBI\_TaxID=10566;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-VS102-4;  
 RC MEDLINE=94340583; PubMed=8062252;  
 RA Shamanin V., Glover M., Rausch C., Proby C., Leigh I.M., zur Hause H.,  
 RA Villiers E.M.,  
 RT "Specific types of HPV found in benign proliferations and carcinomas  
 of the skin in immunosuppressed."  
 RL Cancer Res. 54:4610-4613(1994).  
 DR EMBL: X79946; CAA56294.1; -;  
 DR InterPro; IPR002210; PV\_capsid\_L1.  
 DR Pfam; PF00500; late\_protein\_L1; 1.  
 DR PRINTS; PR00865; HPVcapsidL1.  
 DR PRODOM; PD000544; PV\_capsid\_L1; 1.  
 FT NON\_TER 1  
 FT NON\_TER 224  
 SQ SEQUENCE 224 AA; 24755 MW; 52D6FF377432BEE CRC64;

Query Match 69.5%; Score 41; DB 12; Length 224;  
 Best Local Similarity 69.2%; Pred. No. 4.3;  
 Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 2 LGHPVC 8  
 DB 57 LGHPVC 59  
 DB 57 LGHPVC 59

RESULT 5  
 Q98141 PRELIMINARY; PRT; 404 AA.  
 ID Q98141;  
 AC Q98141; O12570;  
 DT 01-FEB-1997 (TREMBlrel. 02, Created)  
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
 DE ORF 23.  
 OS Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

Query Match 69.5%; Score 41; DB 12; Length 224;  
 Best Local Similarity 69.2%; Pred. No. 4.3;  
 Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 2 LGHPVC 8  
 DB 57 LGHPVC 59  
 DB 57 LGHPVC 59

RESULT 5  
 Q98141 PRELIMINARY; PRT; 404 AA.  
 ID Q98141;  
 AC Q98141; O12570;  
 DT 01-FEB-1997 (TREMBlrel. 02, Created)  
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
 DE ORF 23.  
 OS Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

Query Match 69.5%; Score 41; DB 12; Length 224;  
 Best Local Similarity 69.2%; Pred. No. 4.3;  
 Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 2 LGHPVC 8  
 DB 57 LGHPVC 59  
 DB 57 LGHPVC 59

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OC  Gammarherpesvirinae: Rhadinovirus.
OX  NCBI_TaxID=37296;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=96099469; PubMed=8523568;
RA  Moore P.S., Gao S.J., Dominguez G., Cesarman E., Lungu O.,
RA  Knowles D.M., Garber P., Pellett P.E., McGeoch D.J., Chang Y.;
RT  *Primary characterization of a herpesvirus agent associated with
RT  Kaposi's sarcoma.
RL  J. Virol. 70:549-558(1996).
RN  [2]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=97048116; PubMed=8892957;
RA  Cesarman E., Nador R.G., Bai F., Bohenzky R.A., Russo J.J.,
RA  Moore P.S., Chang Y., Knowles D.M.;
RT  *Kaposi's sarcoma-associated herpesvirus contains G protein-coupled
RT  receptor and cyclin D homologs which are expressed in Kaposi's sarcoma
RT  and malignant lymphoma.
RL  J. Virol. 70:8218-8223(1996).
RN  [3]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=97094384; PubMed=8939871;
RA  Moore P.S., Bashoff C., Weiss R.A., Chang Y.;
RT  *Molecular mimicry of human cytokine and cytokine response pathway
RT  genes by KSHV.
RL  Science 274:1739-1744(1996).
RN  [4]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=97121480; PubMed=8962146;
RA  Russo J.J., Bohenzky R.A., Chien M.C., Chen J., Yan M., Maddalena D.,
RA  Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
RT  *Nucleotide sequence of the Kaposi sarcoma-associated herpesvirus
RT  (HHV8).
RL  Proc. Natl. Acad. Sci. U.S.A. 93:14862-14867(1996).
RN  [5]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=97296220; PubMed=9151804;
RA  Neipel F., Albrecht J.C., Fleckenstein B.;
RT  *Cell-homologous genes in the Kaposi's sarcoma-associated rhadinovirus
RT  human herpesvirus 8: determinants of its pathogenicity?;
RL  J. Virol. 71:4187-4192(1997).
DR  EMBL: U75698; AAC57104.1;
DR  EMBL: U40377; AAB08394.1;
DR  EMBL: U93872; AAB62668.1;
SQ  SEQUENCE 404 AA; 45171 MW; 88B4D2382C97FAE4 CPG64;

Query Match 67.8%; Score 40; DB 12; Length 404;
Best Local Similarity 87.5%; Pred. No. 12; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY  2 LGHPVCD 9
DB  225 LGSPVCD 232
    ||| ||||
    ||| ||||

RESULT 6
Q90W38 PRELIMINARY; PRT: 241 AA.
AC Q90W38;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PUTATIVE NEUTROTROPIC GROWTH FACTOR.

NGF
OS Bothrops jararacussu (Jararacussu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8726;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=VENOM GLAND;
RA Kashima S., Pereira J.O., Astolfi Filho S., Soares A.M.,
RA Cintra A.C.O., Giglio J.R., Franca S.C.;
RT *Molecular cloning and cDNA sequence of a nerve growth factor
RT precursor from Bothrops jararacussu venomous gland.
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY007318; AAG12169.1;
DR EMBL: AY007318; AAG12169.1;
SQ SEQUENCE 241 AA; 27161 MW; AC57F724A6531A8F CPG64;

Query Match 66.1%; Score 39; DB 13; Length 241;
Best Local Similarity 70.0%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY  1 LGHPVCD 10
DB  129 NRGEYSVCD 138
    ||| ||||
    ||| ||||

RESULT 7
Q9XY95 PRELIMINARY; PRT: 324 AA.
AC Q9XY95;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE NEUTROTROPIN.
OS Lampetra fluviatilis (River lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Lampetra.
OX NCBI_TaxID=7748;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=LIVER;
RA MEDLINE=99001404; PubMed=9786977;
RA Hallbook F., Lundin L.G., Kullander K.;
RT *Lampetra fluviatilis neurotrophin homolog, descendant of a
RT neurotrophin ancestor, discloses the early molecular evolution of
RT neurotrophins in the vertebrate subphylum.
RL J. Neurosci. 18:8700-8711(1998).
DR EMBL: AF071432; AAD22744.1;
DR HSSP: P20783; IBBK.
DR InterPro, IPR002072; NGF.
DR Pfam: PF00243; NGF; 1.
DR ProDom: PD002052; NGF; 1.
DR SMART: SM00140; NGF; 1.
DR PROSITE: PS50270; NGF; 2; 1
DR CHAIN 141 324
SQ SEQUENCE 324 AA; 35267 MW; 9D6B56C1978F8485 CPG64;

Query Match 66.1%; Score 39; DB 13; Length 324;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY  3 GEHPVCD 10
DB  177 GEYPACUS 184
    ||| ||||
    ||| ||||

RESULT 8
Q9D468 PRELIMINARY; PRT: 479 AA.
AC Q9D468;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

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DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE 4933411B03RIK PROTEIN.
CN 4933411B03RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaudo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK016763; BAB30415.1; -.
DR HSSP; Q07960; IRGP.
DR MGD; MGI:1918335; 4933411B03RIK.
DR InterPro; IPR000198; RhoGAP.
DR SMART; SM00324; RhoGAP; 1.
SQ SEQUENCE 479 AA, 54025 MW, 3B4A4414EF852424 CP664;

Query Match 66.1%; Score 39; DB 11; Length 479;
Best Local Similarity 87.5%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GERPVCDS 10
DB 9 GERPVCDS 16
|||||

RESULT 9
Q19953 ID Q19953 PRELIMINARY; PRT; 596 AA.
AC Q19953;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 70.0 KDA PROTEIN.
CN F32A5 1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN
RP SEQUENCE FROM N.A.
RX STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN
RP SEQUENCE FROM N.A.
RX STRAIN=BRISTOL N2;
RA Pauley A.;
RT "The sequence of C. elegans cosmid F32A5.";

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RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U20864; AA68355.1; -.
DR InterPro; IPR000822; Znf-C2H2.
DR IuterPro; IPR00249; MYB-DNA-binding; 1.
DR Pfam; PF00249; MYB-DNA-binding; 1.
DR SMART; SM00395; SANT; 1.
DR PROSITE; PS50090; MYB_3; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 596 AA; 69975 MW, 5G26A6A81C0D48E9 CP664;

Query Match 66.1%; Score 39; DB 5; Length 596;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GERPVC 8
DB 19 GERPVC 24
|||||

RESULT 10
Q17490 ID Q17490 PRELIMINARY; PRT; 5170 AA.
AC Q17490;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE B0350 1 PROTEIN
GN B0350.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Phabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Airscough R., Connell M., Baynes C., Herks M.,
RA Bonfield J., Burton J., Durbin R., Pavello A., Fulton L.,
RA Craxton M., Dear S., Du Z., Durbin R., Hillier L., Johnston L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Latreille P.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,
RA Smalton N., Smith A., Sonhammer E., Staden R., Suiston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
RN
RP SEQUENCE FROM N.A.
RX Gattung S.;
RT "The sequence of C. elegans cosmid B0350.";
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U50071; AAA93447.1; -.
SQ SEQUENCE 5170 AA; 575848 MW; 27C2DFBF4AE03A7B CRC64;

Query Match 66.1%; Score 39; DB 5; Length 5170;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 EHPVCDS 10
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Wed Oct 23 14:06:19 2002

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Db 572 EHPACDS 578

RESULT 11
Q17343
ID Q17343 PRELIMINARY: PRT: 6994 AA.
AC Q17343
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE UNC-44 ANKYRINS.
GN UNC-44
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N2;
RX MEDLINE=95263663; PubMed=7744957;
RA Otsuka A.J., Franco R., Yang B., Shim K., Tang L.Z., Zhang Y., V.I.,
RA Boontrakulpoontawee P., Jeyaprakash A., Hedgecock E., Wheaton V.I.,
RA Sobery A.;
RT "An ankyrin-related gene (unc-44) is necessary for proper axonal
RT guidance in Caenorhabditis elegans.";
RL J. Cell Biol. 129:1081-1092(1995).
RN [2]
RP REVISIONS, AND SEQUENCE OF 6126-6994 FROM N.A.
RC STRAIN=N2;
RA Otsuka A.J.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U39847; AAB41827.1; -
DR EMBL: U21733; AAB38384.1; -
DR HSSP: P42773; 11HB.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR000488; Death.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001360; Glyco_hydro_1.
DR InterPro: IPR000906; ZU5.
DR Pfam: PF00023; ank; 24.
DR Pfam: PF00531; death; 1.
DR Pfam: PF00791; ZU5; 1.
DR PRINTS: PR01415; ANKYRIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00248; ANK; 21.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00218; ZU5; 1.
DR PROSITE: PS50088; ANK_REPEAT; 22.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
DR PROSITE: PS00572; GLYCOSYL_HYDROL_F1_1; UNKNOWN_2.
KW ANK repeat; Repeat.
SQ SEQUENCE 6994 AA; 775364 MW; 90CB449925D9923D CRC64;

Query Match 66.1%; Score 39; DB 5; Length 6994;
Best Local Similarity 85.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 EHPACDS 10
DB 2396 EHPACDS 2402

RESULT 12
Q9JUF2
ID Q9JUF2 PRELIMINARY: PRT: 186 AA.
AC Q9JUF2
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE HYPOTHETICAL PROTEIN NMA1343.
GN NMA1343.
OS Neisseria meningitidis (serogroup A).

Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=65699;
[1]
SEQUENCE FROM N.A.
STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;
MEDLINE=20222556; PubMed=10761919;
Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Spratt B.G., Barrall B.G.;
"Complete DNA sequence of a serogroup A strain of Neisseria
meningitidis 22491.";
Nature 404:502-506(2000).
EMBL: AL162755; CAB84591.1; -
InterPro: IPR002110; ANK.
DR SMART: SM00248; ANK; 1.
DR PROSITE: PS50088; ANK_REPEAT; 1.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 186 AA; 21087 MW; 01B85E3FF77DED73 CRC64;

Query Match 64.4%; Score 38; DB 16; Length 186;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 NLGHEPVC 8
DB 98 NLEHPVC 105

RESULT 13
Q9JRZ6
ID Q9JRZ6 PRELIMINARY: PRT: 253 AA.
AC Q9JRZ6;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE CONSERVED HYPOTHETICAL PROTEIN / ANKYRIN-RELATED PROTEIN.
GN NMB1171 AND NMB1133.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WC58 / SEROGROUP B;
MEDLINE=20175755; PubMed=10710307;
RA Tetelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
Mason T., Ciecko A., Parksey D.S., Blair E., Citterone H., Clark E.B.,
Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
Gill J., Scarlato V., Masioni V., Pizzo M., Grandi G., Sun L.,
Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
"Complete genome sequence of Neisseria meningitidis serogroup B strain
MC58.";
Science 287:1809-1815(2000).
DR EMBL: AE002465; AAF41556.1; -
DR EMBL: AE002462; AAF41521.1; -
DR TIGR: NMB1133; -
DR TIGR: NMB1171; -
DR InterPro: IPR002110; ANK.
DR Pfam: PF00023; ank; 1.
DR SMART: SM00248; ANK; 1.
DR PROSITE: PS50088; ANK_REPEAT; 1.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
KW Complete proteome.
SQ SEQUENCE 253 AA; 29197 MW; 989BABI1327B9A44 CRC64;

Query Match 64.4%; Score 38; DB 16; Length 253;
Best Local Similarity 75.0%; Pred. No. 18;

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us-09-613-355d-3\_1.rspt

Wed Oct 23 14:06:19 2002

Query Match 64.4%; Score 38; DB 3; Length 1529;  
 Best Local Similarity 60.0%; Pred. No. 1.2e-02;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLGEHPVCD 10  
 DB 1104 NLQEGICDS 1113

Search completed. October 23, 2002, 12:15:39  
 Job time : 29 secs

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLGEHPVC 8  
 DB 165 NLEHPMC 172

RESULT 14  
 Q19339 PRELIMINARY. PRT: 544 AA.  
 AC Q19339;  
 DT 01-JAN-1999 (TRENBLrel. 09, Created)  
 DT 01-JAN-1999 (TRENBLrel. 09, Last sequence update)  
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
 DE PUTATIVE 4-COUMARATE-COA LIGASE 2 (EC 6.2.1.12) (4CL).  
 GN F1A3.1.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA McMurray A.;  
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ATP + 4-COUMARATE + COA = AMP + PYROPHOSPHATE  
 CC + 4-COUMAROYL-COA.  
 CC -1- PATHWAY: BRANCH-POINT REACTIONS BETWEEN GENERAL PHENYLPROPANOID  
 CC METABOLISM AND PATHWAYS LEADING TO VARIOUS SPECIFIC END PRODUCTS.  
 CC -1- SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT  
 CC COVALENT BINDING OF AMP TO THEIR SUBSTRATE.  
 DR EMBL; Z70751; CAA94751.1;  
 DR HSP; P08659; ILIC1.  
 DR WormPep; F1A3.1; CE05585.  
 DR InterPro; IPR000873; AMP-bind.  
 DR Pfam; PF00501; AMP-binding; 1.  
 DR PROSITE; PS00455; AMP-BINDING; 1.  
 DR Hypothetical protein; Ligase; Phenylpropanoid metabolism.  
 KW SEQUENCE 544 AA; 60306 MW; 74C384771A1A7DFC CRC64;  
 SQ

Query Match 64.4%; Score 38; DB 5; Length 544;  
 Best Local Similarity 62.5%; Pred. NO. 40;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LGEHPVCD 9  
 DB 296 LAKHPICD 303

RESULT 15  
 Q9Y7C6 PRELIMINARY. PRT: 1529 AA.  
 ID Q9Y7C6;  
 AC Q9Y7C6;  
 DT 01-NOV-1999 (TRENBLrel. 12, Created)  
 DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
 DE ESTERASE.  
 OS Aspergillus terreus.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
 OX NCBI\_TaxID=33178;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ATCC20542;  
 RA Kennedy J., Auclair K., Kendrew S.G., Park C., Vederas J.C.,  
 RA Hutchinson C.R.;  
 RT "Accessory Proteins Modulate Polyketide Synthase Activity During  
 RT Lovastatin Biosynthesis."  
 RL Science 0:0-0(1999).  
 DR EMBL; AF141924; AAD34550.1;  
 DR InterPro; IPR001087; Lipase\_GDSL.  
 DR Pfam; PF00657; Lipase\_GDSL; 1.  
 SQ SEQUENCE 1529 AA; 170506 MW; 456FB780A6B531A3 CRC64;



OM protein - protein search, using sw model  
Run on: October 23, 2002, 12:11:14 ; Search time 11 seconds  
(without alignments)  
35.200 Million cell updates/sec

GenCore version 5.1.3  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues  
Total number of hits satisfying chosen parameters. 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

Summary:  
Result No. Score Query Length DB ID Description

Result No.	Score	Query Length	DB ID	Description
1	51	86.4	1	NGF_NAJAT
2	51	86.4	1	NGF_NAJNA
3	45	76.3	1	NGF_BUNMU
4	37	62.7	1	NGF_TOHAC
5	36	61.0	1	NGF_DABRR
6	36	61.0	1	YIA6_YEAST
7	36	61.0	1	YK79_MYCTU
8	36	61.0	1	TOPI_SYNY3
9	35.5	60.2	1	ECT2_MOUSE
10	35.5	60.2	1	ECT2_HUMAN
11	35	59.3	1	NT7_CYPCA
12	35	59.3	1	NT3_CEREL
13	35	59.3	1	NT3_XENLA
14	35	59.3	1	NT7_PPAPF
15	35	59.3	1	NGF_CAVPO
16	35	59.3	1	NGF_MOUSE
17	35	59.3	1	NGF_PAT
18	35	59.3	1	NT3_CHICK
19	35	59.3	1	NT3_HUMAN
20	35	59.3	1	NT3_MOUSE
21	35	59.3	1	NT3_PAT
22	35	59.3	1	NT3_XENLA
23	35	59.3	1	TAM_MYCTU
24	35	59.3	1	ARPI_YEAST
25	35	59.3	1	TRPC_VIBCH
26	35	59.3	1	GLGB_YEAST
27	35	59.3	1	RAPD_TMOB
28	34.5	58.5	1	HFC1_HUMAN
29	34.5	58.5	1	HFC1_MESAU
30	34	57.6	1	MUCA_SALTY
31	34	57.6	1	NGF_PRANA
32	34	57.6	1	YOHI_HAEIN
33	34	57.6	1	ASNS_SCHPO

34 57.6 708 1 RAFA\_ECOLI  
35 57.6 808 1 GCS1\_SCHPO  
36 57.6 1061 1 TRC4\_ECOLI  
37 57.6 2149 1 RPL\_EFVYZ  
38 57.6 3707 1 PGBM\_MOUSE  
39 55.9 107 1 YP94\_YEAST  
40 55.9 299 1 BE46\_SCHPO  
41 55.9 318 1 LPSA\_BACNO  
42 55.9 365 1 RF2\_HAEIN  
43 55.9 389 1 VMSA\_HPBVI  
44 55.9 462 1 RD21\_ARATH  
45 55.9 480 1 UCRL\_MOUSE

# ALIGNMENTS

RESULT 1  
NGF\_NAJAT STANDARD: PRT; 116 AA.

AC P21377;  
DT 01-MAY-1991 (Rel. 18, Created)  
DT 01-MAY-1991 (Rel. 18, Last sequence update)  
DT 01-JUL-1993 (Rel. 26, Last annotation update)  
DE Nerve growth factor (NGF).  
OS Naja atra (Chinese cobra), and  
OS Naja naja kaouthia (Monocled cobra) (Naja naja siamensis).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Elapidae; Elapinae; Naja.  
OX NCBI\_TaxID=8656, 8649;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=N.n. atra; TISSUE=Venom;  
RX MEDLINE=90147847; PubMed=2619756;  
RA Oda T., Ohta M., Inoue S., Ikeda K., Furukawa S., Hayashi K.;  
RT "Amino acid sequence of nerve growth factor purified from the venom  
of the Formosan cobra Naja naja atra.";  
RL Biochem. Int. 19:909-917(1989).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=N.n. kaouthia; TISSUE=Venom;  
RX MEDLINE=91138755; PubMed=1995338;  
RA Inoue S., Oda T., Koyama J., Ikeda K., Hayashi K.;  
RT "Amino acid sequences of nerve growth factors derived from cobra  
venoms.";  
RL FEBS Lett. 279:38-40(1991).  
CC -!- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND  
MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT  
STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND  
EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC  
NEURONS IN THE BRAIN.  
CC -!- SUBUNIT: HOMODIMER.  
CC -!- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
DR PIR, S13965; S13965.  
DR HSP; P01139; 1BET.  
DR InterPro, IPR002400; GF\_CysKnot  
DR InterPro, IPR002072; NGF.  
DR Pfam, PF00243; NGF\_1.  
DR PRINTS; PR00438; GF\_CYSKNOT.  
DR PRINTS; PR00268; NGF.  
DR ProDom; PD002052; NGF; 1.  
DR SMART; SM00140; NGF; 1.  
DR PROSITE; PS00248; NGF\_1; 1  
DR PROSITE; PS00270; NGF\_2; 1.  
KW Growth factor; 14 78 BY SIMILARITY.  
FT DISULFID 56 106 BY SIMILARITY.  
FT DISULFID 56 108 BY SIMILARITY.  
FT DISULFID 56 108 BY SIMILARITY.  
SQ SEQUENCE 116 AA; 13064 MW, DAB35421093F3B06 GRC64;

Query Match 86.4% Score 51; DB 1; Length 116;  
Best Local Similarity 90.0%; Pred. No. 0.01;

us-09-613-355d-3.1.rsp

Wed Oct 23 14:06:18 2002

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Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLGHPVCDs 10
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Db 7 NLGHSVCDs 16

RESULT 2
NGF_NAJNA
ID NGF_NAJNA STANDARD: PRT: 116 AA.
AC P01140:
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Nerve growth factor (NGF).
OS Naja naja (Indian cobra).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Elapinae; Naja.
OX NCBI_TaxID=35670;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom.
RA Inoue S., Oda T., Koyama J., Ikeda K., Hayashi K.;
RT "Amino acid sequences of nerve growth factors derived from cobra
venoms.";
RL FEBS Lett. 279:38-40(1991).
RN [2]
RP PRELIMINARY SEQUENCE.
RC TISSUE=Venom;
RA Hoque-Angeletti R.A., Frazier W.A., Jacobs J.W., Niall H.D.,
RT Bradshaw R.A.;
RT "Purification, characterization, and partial amino acid sequence of
nerve growth factor from cobra venom.";
RL Biochemistry 15:26-34(1976).
CC -!- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
NEURONS IN THE BRAIN.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SIMILARITY: BELONGS TO THE NCF-BETA FAMILY.
DR PIR: A01401; NGNXXI.
DR PIR: S13927; S13927.
DR HSSP: P01139; 1BET.
DR InterPro: IPR002400; GF_cysknot.
DR Pfam: PF00243; NGF; 1.
DR PRINTS: PR00243; NGF; 1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS0270; NGF_2; 1.
DR PROSITE: PS0268; NGF.
DR PRINTS: PR00243; GPCYSKNOT.
DR PRINTS: PR00268; NGF.
DR PRODOM: PD002052; NGF; 1.
DR SMART: SM00140; NGF; 1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS0270; NGF_2; 1.
KW Growth factor.
FT DISULFID 14 78 BY SIMILARITY.
FT DISULFID 56 106 BY SIMILARITY.
FT DISULFID 66 108 BY SIMILARITY.
SQ SEQUENCE 116 AA; 13022 MW; DAB346B1093E7E06 CRC64;

Query Match 86.4%; Score 51; DB 1; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.01;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NLGHPVCDs 10
    ||||| ||||
Db 7 NLGHSVCDs 16

RESULT 3
NGF_BUNMU
ID NGF_BUNMU STANDARD: PRT: 243 AA.
AC P34128;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Nerve growth factor precursor (NGF).
OS Bungarus multicinctus (Many-banded krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Bungarinae; Bungarus.
OX NCBI_TaxID=8616;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom;
RA Danse J.M., Garnier J.M.;
RT "Molecular cloning of a cDNA encoding a nerve growth factor precursor
from the krait, Bungarus multicinctus.";
RL Growth Factors 8:77-86(1993).
CC -!- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
NEURONS IN THE BRAIN.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SIMILARITY: BELONGS TO THE NCF-BETA FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
DR EMBL: S56212; AAB25729.1; -.
DR HSSP: P01139; 1BET.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF; 1.
DR PRODOM: PD002052; NGF; 1.
DR SMART: SM00140; NGF; 1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS0270; NGF_2; 1.
DR PROSITE: PS0268; NGF.
KW Growth factor; Signal.
FT SIGNAL 1 18
FT PROPEP 19 125
FT CHAIN 126 243 NERVE GROWTH FACTOR
FT DISULFID 139 204 BY SIMILARITY.
FT DISULFID 182 232 BY SIMILARITY.
FT DISULFID 192 234 BY SIMILARITY.
SQ SEQUENCE 243 AA; 27514 MW; E33F64B142179A08 CRC64;

Query Match 76.3%; Score 45; DB 1; Length 243;
Best Local Similarity 80.0%; Pred. No. 0.28;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NLGHPVCDs 10
    ||||| ||||
Db 132 NLGHSVCDs 141

RESULT 4
NTF6_TOBAC
ID NTF6_TOBAC STANDARD: PRT: 371 AA.
AC Q40531;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Mitogen-activated protein kinase homolog NTF6 (EC 2.7.1.1) (P43).
DE Nicotiana tabacum (Common tobacco).
OS Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;

```

SEQUENCE.

PC TISSUE-Venom; PubMed-1477101; Hayashi K.;

RX MEDLINE-9320151; Inoue S., Ikeda K., Hayashi K.;

RA Koyama J.-I., Inoue S., Ikeda K., Hayashi K.;

RT "Purification and amino-acid sequence of a nerve growth factor from

KL Blochim. Biophys. Acta 1160:287-292(1992).

CC -!- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND

CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT

CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND

CC EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC

CC NEURONS IN THE BRAIN.

CC -!- SUBUNIT: HOMODIMER.

CC -!- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.

DR PIR: S28161; S28161.

DR HSP: P01149; IBET.

DR InterPro: IPR002072; NGF.

DR Pfam: PF00243; NGF; 1.

DR PRINTS: P00268; NGF; 1.

DR PRODOM: PD002052; NGF; 1.

DR SMART: SM00140; NGF; 1.

DR PROSITE: PS00248; NGF\_1; 1.

DR PROSITE: PS00270; NGF\_2; 1.

KW Glycoprotein; Growth factor.

FT DISULFID 12 77 BY SIMILARITY.

FT DISULFID 55 105 BY SIMILARITY.

FT DISULFID 65 107 BY SIMILARITY.

FT CARBOHYD 21 21 N-LINKED (GLCNAC...).

SQ SEQUENCE 117 AA, 13283 MW, A6459C5FC11F66 CPC64;

Query Match 61.0%; Score 36; DB 1; Length 117;

Best Local Similarity 70.0%; Pred. No. 6.3;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NLGHPVCDs 10

Db 5 NQGEFSVCDs 14

RESULT 6

VIA6\_YEAST STANDARD; PRT; 373 AA.

ID YIA6\_YEAST

AC P40556;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 01-FEB-1995 (Rel. 31, Last annotation update)

DE Putative mitochondrial carrier YIL006W.

OS YIL006W.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

OX NCBI\_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN-S288C / AB972;

RC Barrell B.G., Badcock K., Bankier A.T., Bowden S., Brown D.,

RA Churcher C.M., Connor R., Copsey T.S., Dear S., Devlin K., Fraser A.,

RA Gentles S., Hamlyn N., Harsnall T.S., Hunt S., Javelis K., Jones M.,

RA Louis E., Lye G., Moule T., Odell C., Pearson D.,

RA Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,

RA Walsh S.V., Whitehead S.;

RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial

CC inner membrane (potential).

CC -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

CC -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

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CC

SPERMATOPHYTES; Magnoliophyta; eudicotyledons; core eudicots;

AC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.

NCBI\_TaxID=4097;

SEQUENCE FROM N.A.

STRAIN-CV PETIT HAVANA SRI;

MEDLINE-9601956; PubMed-7588752;

Wilson C., Anglmayer R., Vicente O., Heberle-Bors E.;

"Molecular cloning, functional expression in Escherichia coli, and

characterization of multiple mitogen-activated-protein kinases from

tobacco".

Eur. J. Biochem. 233:249-257(1995).

-!- ENZYME REGULATION: ACTIVATED BY TYROSINE AND THREONINE

PHOSPHORYLATION (BY SIMILARITY).

-!- PTM: VERY LOW AUTOPHOSPHORYLATION. ALTHOUGH DRAMATICALLY INCREASED

WHEN MN2+ IS ADDED TO THE REACTION INSTEAD OF MG2+.

-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

MAP KINASE SUBFAMILY.

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EMBL: X83879; CAA58760.1; -

HSP: Q16539; LWFC.

InterPro: IPR000719; Euk\_pkinase.

InterPro: IPR003527; MAP\_kin.

InterPro: IPR002290; Ser\_thr\_kinase

Pfam: PF00069; pkinase; 1.

SMART: SM00220; S\_TKC; 1.

PROSITE: PS01351; MAPK; 1.

PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.

PROSITE: PS00111; PROTEIN\_KINASE\_DOM; 1.

PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.

Transferase: Serine/threonine-protein kinase: ATP-binding;

Phosphorylation; Multigene family.

DOMAIN 38 324 PROTEIN KINASE.

NP\_BIND 44 52 ATP (BY SIMILARITY).

BINDING 67 67 ATP (BY SIMILARITY).

BY SIMILARITY.

ACT\_SITE 164 164 PHOSPHORYLATION (ACTIVATES THE KINASE)

MOD\_RES 196 196 (BY SIMILARITY).

MOD\_RES 198 198 PHOSPHORYLATION (ACTIVATES THE KINASE)

(BY SIMILARITY).

SEQUENCE 371 AA, 42741 MW, 4D97C41AC303C272 CRC64;

Query Match 62.7%; Score 37; DB 1; Length 371;

Best Local Similarity 66.7%; Pred. No. 13;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LGHPVCDs 10

Db 330 INEEPVDs 338

RESULT 5

NGF\_DABRR STANDARD; PRT; 117 AA.

ID NGF\_DABRR

AC P30894;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Nerve growth factor (NGF).

OS Dabolia russelli russelli (Russell's viper) (Vipera russelli russelli).

OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidae;

OC Viperidae; Viperinae; Daboia.

OX NCBI\_TaxID=31159;

RN [1]

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CC
CC EMBL: Z38113; CAA86245.1; -.
CC PIR: S48451; S48451.
CC SCD: S0001268; YIL006W.
CC InterPro: IPR001993; Mitoch_carrier.
CC Pfam: PF00153; mito_car1; 3.
CC PROSITE: PS00215; MITOCH_CARRIER; 2.
CC KW Hypothetical protein; Mitochondrion; Inner membrane; Repeat;
CC Transmembrane; Transport.
CC TRANSMEM 81 101 POTENTIAL.
CC TRANSMEM 142 162 POTENTIAL.
CC TRANSMEM 166 186 POTENTIAL.
CC TRANSMEM 236 256 POTENTIAL.
CC SQ SEQUENCE 373 AA; 41954 MW; 976C767C1D40E8DF CRC64;

Query Match 61.0%; Score 36; DB 1; Length 373;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGEHP 6
DB 209 NLGEHP 214

RESULT 7
YK79_MYCTU STANDARD; PRT; 656 AA.
ID YK79_MYCTU
AC Q10687;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 69.8 kDa protein Rv2079.
GN RV2079 OR MT2140 OR MTCY49.18.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N A
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brusch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeyer K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor K.,
RA Davies K., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares K.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RA "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N A.
RX STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kjolund J.F., Nelson W.C., Mayhew J.A., McLaughlin S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RA "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: SOME, TO M.TUBERCULOSIS RV0963C.
-----
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us-09-613-355d-3\_1.rsp

Wed Oct 23 14:06:18 2002

KW Guanine-nucleotide releasing factor; Repeat; Proto-oncogene.  
 FT DOMAIN 1 76 BRCT 1.  
 FT DOMAIN 91 179 BRCT 2.  
 FT DOMAIN 277 466 DH.  
 FT DOMAIN 500 619 PH.  
 SQ SEQUENCE 738 AA; 83685 MW, 3D279C8F1570C681 C7F64;  
 Query Match 60.2%; Score 35.5; DB 1; Length 738;  
 Best Local Similarity 77.8%; Pred. No. 49;  
 Matches 7; Conservative 1; Mismatches 0; Indels 1; Gaps 1;  
 QY 1 NLGEHPVCD 9  
 :|||||  
 Db 505 SLGEHP-CD 512

RESULT 10  
 ECT2\_HUMAN STANDARD; PRT; 883 AA.  
 ID ECT2\_HUMAN Q9H8V3; Q9NVW9; Q9NSV8;  
 AC Q9H8V3; Q9NVW9; Q9NSV8;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE ECT2 protein (Epithelial cell transforming sequence 2 oncogene).  
 GN ECT2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
 RA Nishikawa T., Naga K., Sugano S., Aotsuka S., Yoshikawa Y.,  
 RA Matsunawa Y., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,  
 RA Nakamura Y., Nagahara K., Masuho Y., Sasaki N.,  
 RT "NEDO human cDNA sequencing project."  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 631-883 FROM N.A.  
 RC TISSUE=Testis;  
 RA Blum H., Bauersachs S., Mewes H.-W., Gassenhuber J., Wiemann S.;  
 RA Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: BINDS HIGHLY SPECIFICALLY TO RHOA, PHOC AND RAC  
 CC PROTEINS, BUT DOES NOT APPEAR TO CATALYZE GUANINE NUCLEOTIDE  
 CC EXCHANGE (By similarity).  
 CC -1- SIMILARITY: CONTAINS 2 BRCT DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY DOMAIN (DH).  
 CC -1- CAUTION: It is uncertain whether Met-1 or Met-146 is the  
 CC Initiator.  
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 CC EMBL; AK023267; BAB14498.1;  
 CC EMBL; AK01323; BAA91624.1;  
 CC EMBL; AL137710; CAB70886.1;  
 CC MIM; 600586;  
 CC InterPro; IPR001357; BRCT.  
 CC InterPro; IPR001331; GDS\_CDC24.  
 CC InterPro; IPR001849; PH.  
 CC InterPro; IPR000219; RHOGEF.  
 CC Pfam; PF00533; BRCT; 2.  
 CC Pfam; PF00621; RHOGEF; 1.  
 CC SMART; SM00292; BRCT; 2.  
 CC SMART; SM00293; PH; 1.  
 CC SMART; SM00325; RHOGEF; 1.  
 CC PROSITE; PS50172; BRCT; 2.

DR SMART; SM00436; TOP1bc; 1.  
 DR SMART; SM00493; TOP1PR; 1.  
 DR PROSITE; PS00396; TOPOISOMERASE\_I\_PROK; 1.  
 KW Isomerase; Topoisomerase; DNA binding; Complete proteome.  
 FT ACT\_SITE 320 330 DNA\_CLEAVAGE (BY SIMILARITY)  
 SQ SEQUENCE 898 AA; 99340 MW, 9416665977398EB3 CRC64;  
 Query Match 61.0%; Score 36; DB 1; Length 898;  
 Best Local Similarity 100.0%; Pred. No. 48;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 NLGEHP 6  
 :|||||  
 Db 721 NLGEHP 726

RESULT 9  
 ECT2\_MOUSE STANDARD; PRT; 738 AA.  
 ID ECT2\_MOUSE Q07139;  
 AC Q07139;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE ECT2 protein (Epithelial cell transforming sequence 2 oncogene).  
 GN ECT2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE; 93218723; PubMed=8464478;  
 RA Miki T., Smith C.L., Long J.E., Eva A., Fleming T.P.;  
 RT "Oncogene ect2 is related to regulators of small GTP-binding  
 RT proteins.";  
 RL Nature 362:462-465(1993).  
 RN [2]  
 RP ERRATUM.  
 RA Miki T., Smith C.L., Long J.E., Eva A., Fleming T.P.;  
 RL Nature 364:737-737(1993).  
 CC -1- FUNCTION: BINDS HIGHLY SPECIFICALLY TO RHOA, PHOC AND RAC  
 CC PROTEINS, BUT DOES NOT APPEAR TO CATALYZE GUANINE NUCLEOTIDE  
 CC EXCHANGE. TRUNCATION OF THE N-TERMINUS PUTS THE PROTEIN IN AN  
 CC ACTIVATED STATE.  
 CC -1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN TESTIS. ALSO DETECTABLE  
 CC IN KIDNEY, LIVER AND SPLEEN.  
 CC -1- SIMILARITY: CONTAINS 2 BRCT DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY DOMAIN (DH).  
 CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.  
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 CC EMBL; L11316; AAA37536.1;  
 CC MGD; MG1:95281; ECT2.  
 CC InterPro; IPR001357; BRCT.  
 CC InterPro; IPR001331; GDS\_CDC24.  
 CC InterPro; IPR001849; PH.  
 CC InterPro; IPR000219; RHOGEF.  
 CC Pfam; PF00533; BRCT; 2.  
 CC Pfam; PF00621; RHOGEF; 1.  
 CC SMART; SM00292; BRCT; 2.  
 CC SMART; SM00293; PH; 1.  
 CC SMART; SM00325; RHOGEF; 1.  
 CC PROSITE; PS50172; BRCT; 2.  
 CC PROSITE; PS50010; DH; 1.  
 CC PROSITE; PS00741; DH; 1.  
 CC PROSITE; PS50003; PH\_DOMAIN; 1.

us-09-613-355d-3\_1.rsp

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DR PROSITE: PS00010; DH_2: 1.
DR PROSITE: PS00741; DH_1: 1.
DR PROSITE: PS00003; PH_DOMAIN: FALSE_NEG.
KW Guanine-nucleotide releasing BRCT 1.
FT DOMAIN 140 229 BRCT 2.
FT DOMAIN 235 323 DH.
FT DOMAIN 421 610 PH.
FT DOMAIN 644 763
FT CONFLICT 855 883
FT
FT
SQ SEQUENCE 883 AA, 100059 MW, 156F4DAF717364DD CRC64:

Query Match 59.3%; Score 35.5; DB 1; Length 883;
Best Local Similarity 77.8%; Pred. No. 59;
Matches 7; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 NLGHPVCD 9
Db 649 SLGHP-CD 656

RESULT 11
NT7_CYPCA STANDARD: PRT: 140 AA.
AC 09474:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Neurotrophin-7 precursor (NT-7) (Fragment).
GN NT7 OR NT7 OR NNT.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=9618228;
RA Lai K.-O., Fu W.-Y., Ip F.C.F., Ip N.Y.;
RT "Cloning and expression of a novel neurotrophin, NT-7, from carp.";
RL Mol. Cell. Neurosci. 11:64-76(1998).
CC
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC
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CC
CC EMBL: U94949, AAC25632.1; -.
CC HSSP: P01139, 1BTG.
CC InterPro: IPR002072; NGF.
CC Pfam: PF00243; NGF; 1.
CC PRINTS: PR00268; NGF.
CC ProDom: PD002052; NGF; 1.
CC SMART: SM00140; NGF; 1.
CC PROSITE: PS00248; NGF_1; 1.
CC PROSITE: PS50270; NGF_2; 1.
CC Growth factor.
CC NON_TER 1 1
CC PROPEP <1 7
CC CHAIN 8 140
CC DISULFID 21 101
CC DISULFID 64 129
CC DISULFID 89 131
CC VARIANT 70 70 I -> V.
CC VARIANT 95 95 E -> K.
CC SEQUENCE 140 AA; 15855 MW; 3F5E0BCE2601B0FC CRC64;

Query Match 59.3%; Score 35; DB 1; Length 140;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 3 GEHPVCD 10
Db 16 GEYSVCD 23

RESULT 12
NT3_CEREL STANDARD: PRT: 154 AA.
AC 095150:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Neurotrophin-3 precursor (NT-3) (Fragment).
GN NTF3.
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Antler;
RX MEDLINE=98001474; PubMed=9343309;
RA Garcia R.L., Sadiqhi M., Francis S.M., Suttie J.M., Fleming J.S.;
RT "Expression of neurotrophin-3 in the growing velvet antler of the red
RT deer Cervus elaphus.".
RL J. Mol. Endocrinol. 19:173-182(1997).
CC
CC -1- FUNCTION: SEEMS TO PROMOTES THE SURVIVAL OF VISCERAL AND
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC
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CC
CC EMBL: U66715, AAB07024.1; -.
CC HSSP: P20783; 1B8K.
CC InterPro: IPR002072; NGF.
CC Pfam: PF00243; NGF; 1.
CC PROSITE: PS00248; NGF_1; PARTIAL.
CC PROSITE: PS50270; NGF_2; PARTIAL.
CC Growth factor; Signal.
CC SIGNAL 1 18
CC PROPEP 19 134 BY SIMILARITY.
CC CHAIN 135 >154 NEUROTROPHIN-3.
CC NON_TER 154 154
CC SEQUENCE 154 AA; 17858 MW; 0EB36CC52E172CCD CRC64;

Query Match 59.3%; Score 35; DB 1; Length 154;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 3 GEHPVCD 10
Db 143 GEYSVCD 150

RESULT 13
NGF_XENLA STANDARD: PRT: 231 AA.
AC P21617;
DT 01-MAY-1991 (Rel. 18, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)

```

DE Nerve growth factor precursor (NGF).  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91362944; PubMed=1888511;  
RA Carriero F., Campioni M., Cardinali B., Pierandrei-Analdi P.:  
RT "Structure and expression of the nerve growth factor gene in Xenopus  
RT oocytes and embryos."  
RL Mol. Repr. Dev. 29:313-322(1991).  
RN [2]  
RP SEQUENCE OF 170-211 FROM N.A.  
RX TISSUE=Liver.  
RA MEDLINE=9122573; PubMed=2025430;  
RA Hallboeek F., Ibanez C.F., Perisson H.:  
RT "Evolutionary studies of the nerve growth factor family reveal a  
RT novel member abundantly expressed in Xenopus ovary."  
RL Neuron 6:845-858(1991).  
CC -!- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND  
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT  
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND  
CC EMBRYONIC SENSORY NEURONS.  
CC -!- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES  
CC -!- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
CC -----  
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CC -----  
DR EMBL: X55716; CAA39249.1; ALT\_INIT.  
DR PIR: S14481; S14481.  
DR HSP: P01139; IBET.  
DR InterPro: IPR002072; NGF.  
DR Pfam: PF00243; NGF; 1.  
DR PRINTS: P00268; NGF.  
DR ProDom: PD002052; NGF; 1.  
DR SMART: SM00140; NGF; 1.  
DR PROSITE: PS00248; NGF\_1; 1.  
DR PROSITE: PS50270; NGF\_2; 1.  
DR Growth factor; Signal.  
KW SIGNAL 1 18  
FT PROPEP 19 114  
FT CHAIN 115 231  
FT DISULFID 128 193  
FT DISULFID 171 221  
FT DISULFID 181 223  
FT CARBOHYD 63 63  
FT CARBOHYD 107 107  
FT CARBOHYD 158 158  
FT CARBOHYD 158 158  
SQ SEQUENCE 231 AA; 26416 MW; 72A04E7D00B858C5 CRC64;  
Query Match 59.3%; Score 35; DB 1; Length 231;  
Best Local Similarity 75.0%; Pred. No. 19;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 3 GEHPVCDS 10  
DB 123 GEYSVCS 130  
II: |||||  
RESULT 14  
NT7\_BRARE  
ID NT7\_BRARE STANDARD; PRT; 233 AA.  
AC 073797;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Neurotrophin-7 precursor (NT-7) (ZNT-7).  
GN NT7 OF NT7.  
OS Brachydanio rerio (Zebrafish) (Zebra danio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
OC Cypriniformes; Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9819571; PubMed=9580190;  
RA Nilsson A.-S., Fainzilber M., Falck P., Ibanez C.F.:  
RT "Neurotrophin-7: a novel member of the neurotrophin family from the  
RT zebrafish."  
RL FEBS Lett. 424:285-290(1998).  
CC -!- FUNCTION: RECOMBINANT ZNT-7 WAS ABLE TO BIND TO THE HUMAN P75  
CC NEUROTROPHIN RECEPTOR AND TO INDUCE TYROSINE PHOSPHORYLATION OF  
CC THE RAT TRKA RECEPTOR TYROSINE KINASE, ALBEIT LESS EFFICIENTLY  
CC THAN RAT NGF. ZNT-7 DID NOT INTERACT WITH RAT TRKB OR TRAC,  
CC INDICATING A SIMILAR RECEPTOR SPECIFICITY AS NGF.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: AF05906; AAC41272.1; -.  
DR HSP: P01139; IBET.  
DR ZFIN: ZDB-GENE-990415-176; nt7f.  
DR InterPro: IPR002072; NGF.  
DR Pfam: PF00243; NGF; 1.  
DR PRINTS: P00268; NGF.  
DR ProDom: PD002052; NGF; 1.  
DR SMART: SM00140; NGF; 1.  
DR PROSITE: PS00248; NGF\_1; 1.  
DR PROSITE: PS50270; NGF\_2; 1.  
DR Growth factor; Signal.  
KW SIGNAL 1 19  
FT PROPEP 20 97  
FT CHAIN 98 233  
FT DISULFID 110 190  
FT DISULFID 153 218  
FT DISULFID 178 220  
FT DISULFID 178 220  
SQ SEQUENCE 233 AA; 26423 MW; AD0FCE96DF52C454 CRC64;  
Query Match 59.3%; Score 35; DB 1; Length 233;  
Best Local Similarity 75.0%; Pred. No. 19;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 3 GEHPVCDS 10  
DB 105 GEYSVCS 112  
II: |||||  
RESULT 15  
NGF\_CAVPO  
ID NGF\_CAVPO STANDARD; PRT; 241 AA.  
AC P19093;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE Beta-nerve growth factor precursor (Beta-NGF).  
GN NGFB.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]

us-09-613-355d-3\_1.rsp

Wed Oct 23 14:06:18 2002

HP SEQUENCE FROM N.A.  
 KC TISSUE-Prostate;  
 RX MEDLINE-89177243; PubMed-2926397;  
 RA Schwarz M.A., Fisher D., Bradshaw R.A., Isackson P.J.;  
 RT "Isolation and sequence of a cDNA clone of beta-nerve growth factor  
 from the guinea pig prostate gland.";  
 RL J. Neurochem. 52:1203-1209(1989).  
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND  
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT  
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND  
 CC EMBRYONIC SENSORY NEURONS.  
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.  
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.  
 DR PIR: JLO097; JLO097.  
 DR HSP: P01139; IBET.  
 DR InterPro: IPR002072; NGF.  
 DR Pfam: PF00243; NGF; 1.  
 DR PRINTS: PR00268; NGF.  
 DR PRODOM: PD002052; NGF; 1.  
 DR SMART: SM00140; NGF; 1.  
 DR PROSITE: PS00248; NGF\_1; 1.  
 DR PROSITE: PS00270; NGF\_2; 1.  
 KW Growth factor; Signal.  
 FT SIGNAL 1 18 POTENTIAL.  
 FT PROPEP 19 121 BETA-NERVE GROWTH FACTOR.  
 FT CHAIN 122 241 BY SIMILARITY.  
 FT DISULFID 136 201 BY SIMILARITY.  
 FT DISULFID 179 229 BY SIMILARITY.  
 FT DISULFID 189 231 BY SIMILARITY.  
 FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 241 AA, 26821 MW, 2F4E26E197804RF4 CPC64;

Query Match 59.3%; Score 35; DB 1; Length 241;  
 Best Local Similarity 60.0%; Pred. No. 20;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 NLGHPVCD5 10  
 DB 129 HMGFSVCDS 138

Search completed, October 23, 2002, 12:15:05  
 Job time : 13 secs



Oct 23 14:06:17 2002

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 23, 2002, 12:13:29 : Search time 16 seconds  
(without alignments)  
60.056 Million cell updates/sec

Title: US-09-613-355d-3  
Perfect score: 59  
Sequence: 1 NLGHPVCDS 10

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283138 seqs, 96089334 residues 283138

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR.71.\*

1: PIR1.\*  
2: PIR2.\*  
3: PIR3.\*  
4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	86.4	116	1 NGNXXI	nerve growth facto
2	51	86.4	116	2 A58566	nerve growth facto
3	51	86.4	246	2 A59218	nerve growth facto
4	45	76.3	243	2 I51193	nerve growth facto
5	41	69.5	224	2 S48779	L1 protein - human
6	39	66.1	925	2 T16235	hypothetical prote
7	39	66.1	5170	2 T15348	hypothetical prote
8	38	64.4	186	2 C81903	hypothetical prote
9	38	64.4	253	2 D81118	conserved hypothet
10	38	64.4	544	2 T20741	hypothetical prote
11	37	62.7	116	2 J07620	guanylin precursor
12	37	62.7	371	2 S51320	mitogen-activated
13	37	62.7	1317	2 B41950	retrovirus-related
14	36	61.0	117	2 S28161	nerve growth facto
15	36	61.0	373	2 J48451	probable membrane
16	36	61.0	454	2 J48448	cysteine proteinas
17	36	61.0	656	2 B70766	hypothetical prote
18	36	61.0	676	2 B85107	hypothetical prote
19	36	61.0	705	2 T04052	hypothetical prote
20	36	61.0	898	2 S74903	DNA topoisomerase
21	36	61.0	1529	2 T02730	RNA-directed DNA p
22	36	61.0	1747	2 AC1842	WD-40 repeat prote
23	35.5	60.2	297	2 T46414	hypothetical prote
24	35.5	60.2	738	2 S32372	transforming prote
25	35	59.3	235	2 S14481	nerve growth facto
26	35	59.3	241	2 JL0097	nerve growth facto
27	35	59.3	245	2 I56570	beta-nerve growth
28	35	59.3	257	2 C40304	neurotrophin-3 pre
29	35	59.3	257	2 I50400	neurotrophin-3 pre

## ALIGNMENTS

### RESULT 1

NGNXXI

C:Species: Naja naja naja (Indian cobra)

C>Date: 30-Nov-1980 #sequence\_revision 25-Apr-1997 #text\_change 17 Mar-2000

C:Accession: S13927; A01401

R:Inoue, S.; Oda, T.; Koyama, J.; Ikeda, K.; Hayashi, K.

FEBS Lett. 279, 38-40, 1991

A:Title: Amino acid sequences of nerve growth factors derived from cobra venoms.

A:Reference number: S13927; MUID:91138755

A:Accession: S13927

A:Molecule type: protein

A:Residues: 1-116<INO>

A:Experimental source: venom

A:Note: the source is designated as Naja naja and referred to as Indian cobra, so we

P:Hoque-Angelletti, R.A.; Frazier, W.A.; Jacobs, J.W.; Niall, H.D.; Bradshaw, R.A.

Biochemistry 15, 26-34, 1976

A:Title: Purification, characterization, and partial amino acid sequence of nerve gro

A:Reference number: A01401; MUID:76114772

A:Accession: A01401

A:Molecule type: protein

A:Residues: 1-11, P', L3-14, 'B', 16, 'TBT', 20-21, 'GV', 23-27, 'N', 29-31, 'AS', 34, 'S', 36-48,

15-116<HOG>

A:Experimental source: venom

A:Note: the source is designated as Naja naja and referred to as Indian cobra, so we

C:Comment: Nerve growth factor is necessary for the development of embryonic sympathetic

C:Complex: homodimer

C:Superfamily: nerve growth factor beta chain

C:Keywords: growth factor; homodimer; venom

F:14-78,56-106,66-108/Disulfide bonds: #status predicted

Query Match 86.4%; Score 51; DB 1; Length 116;

Best Local Similarity 90.0%; Pred. No. 0 035; 1; Indels 0;

Matches 9, Conservative 0; Mismatches 1; Gaps 0;

Qy 1 NLGHPVCDS 10

Db 7 NLGHPVCDS 16

### RESULT 2

A58566

C:Species: Naja naja atra (Chinese cobra)

C>Date: 16-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 25-Apr-1997

C:Accession: A58566

P:Oda, T.; Ohta, M.; Inoue, S.; Ikeda, K.; Furukawa, S.; Hayashi, K.

Biochem. Int. 19, 909-917, 1989

A:Title: Amino acid sequence of nerve growth factor purified from the venom of the

A:Reference number: A58566; MUID:90147847

A:Accession: A58566

A:Molecule type: protein

```

A:Residues: 1-116 <QDA>
A:Experimental source: venom
C:Comment: Nerve growth factor is necessary for the development of embryonic sympathetic
C:Complex: homodimer
C:Superfamily: nerve growth factor beta chain
C:Keywords: growth factor; homodimer; venom
F:14-78,56-106,66-108/Disulfide bonds: #status predicted

Query Match      86.4%; Score 51; DB 2; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.035;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLGHPVCDs 10
Db 7 NLGHSVCDs 16

RESULT 3
A59218
nerve growth factor beta chain precursor - monocled cobra
C:Species: Naja naja kaouthia, Naja naja siamensis (monocled cobra)
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000
C:Accession: A59218; S13965
R:Seiby, M.J.; Edwards, R.H.; Rutter, W.J.
J. Neurosci. Res. 18, 293-298, 1987
A:Title: Cobra nerve growth factor: structure and evolutionary comparison.
A:Reference number: A59218; MUID:88090976
A:Accession: A59218
A:Molecule type: mRNA
A:Residues: 1-246 <SEL>
R:Inoue, S.; Oda, T.; Koyama, J.; Ikeda, K.; Hayashi, K.
FEBS Lett. 279, 38-40, 1991
A:Title: Amino acid sequences of nerve growth factors derived from cobra venoms.
A:Reference number: S13927; MUID:91138755
A:Accession: S13965
A:Molecule type: protein
A:Residues: 131-246 <INO>
A:Experimental source: venom
C:Comment: Nerve growth factor is necessary for the development of embryonic sympathetic
C:Complex: homodimer
C:Superfamily: nerve growth factor beta chain
C:Keywords: growth factor; homodimer; venom
F:1-23/Domain: signal sequence #status predicted <SIG>
F:131-246/Product: nerve growth factor beta chain #status experimental <MAT>
F:144-208,186-236,196-238/Disulfide bonds: #status predicted

Query Match      86.4%; Score 51; DB 2; Length 246;
Best Local Similarity 90.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLGHPVCDs 10
Db 137 NLGHSVCDs 146

RESULT 4
I51193
nerve growth factor precursor - many-banded krait
C:Species: Bungarus multicinctus (many-banded krait)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C:Accession: I51193
R:Banse, J.M.; Garnier, J.M.
Growth Factors 8, 77-86, 1993
A:Title: Molecular cloning of a cDNA encoding a nerve growth factor precursor from the
A:Reference number: I51193; MUID:93192074
A:Accession: I51193
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-243 <DAN>
A:Cross-references: GB:S5612, NID:q566298; PDB: AAB25729.1; PDB:q566299
C:Superfamily: nerve growth factor beta chain

Query Match      76.3%; Score 45; DB 2; Length 243;

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A:Residues: 1-116 <QDA>
A:Experimental source: venom
C:Comment: Nerve growth factor is necessary for the development of embryonic sympathetic
C:Complex: homodimer
C:Superfamily: nerve growth factor beta chain
C:Keywords: growth factor; homodimer; venom
F:14-78,56-106,66-108/Disulfide bonds: #status predicted

Query Match      86.4%; Score 51; DB 2; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.035;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLGHPVCDs 10
Db 7 NLGHSVCDs 16

RESULT 3
A59218
nerve growth factor beta chain precursor - monocled cobra
C:Species: Naja naja kaouthia, Naja naja siamensis (monocled cobra)
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000
C:Accession: A59218; S13965
R:Seiby, M.J.; Edwards, R.H.; Rutter, W.J.
J. Neurosci. Res. 18, 293-298, 1987
A:Title: Cobra nerve growth factor: structure and evolutionary comparison.
A:Reference number: A59218; MUID:88090976
A:Accession: A59218
A:Molecule type: mRNA
A:Residues: 1-246 <SEL>
R:Inoue, S.; Oda, T.; Koyama, J.; Ikeda, K.; Hayashi, K.
FEBS Lett. 279, 38-40, 1991
A:Title: Amino acid sequences of nerve growth factors derived from cobra venoms.
A:Reference number: S13927; MUID:91138755
A:Accession: S13965
A:Molecule type: protein
A:Residues: 131-246 <INO>
A:Experimental source: venom
C:Comment: Nerve growth factor is necessary for the development of embryonic sympathetic
C:Complex: homodimer
C:Superfamily: nerve growth factor beta chain
C:Keywords: growth factor; homodimer; venom
F:1-23/Domain: signal sequence #status predicted <SIG>
F:131-246/Product: nerve growth factor beta chain #status experimental <MAT>
F:144-208,186-236,196-238/Disulfide bonds: #status predicted

Query Match      86.4%; Score 51; DB 2; Length 246;
Best Local Similarity 90.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLGHPVCDs 10
Db 137 NLGHSVCDs 146

RESULT 4
I51193
nerve growth factor precursor - many-banded krait
C:Species: Bungarus multicinctus (many-banded krait)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C:Accession: I51193
R:Banse, J.M.; Garnier, J.M.
Growth Factors 8, 77-86, 1993
A:Title: Molecular cloning of a cDNA encoding a nerve growth factor precursor from the
A:Reference number: I51193; MUID:93192074
A:Accession: I51193
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-243 <DAN>
A:Cross-references: GB:S5612, NID:q566298; PDB: AAB25729.1; PDB:q566299
C:Superfamily: nerve growth factor beta chain

Query Match      76.3%; Score 45; DB 2; Length 243;

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Best Local Similarity 80.0%; Pred. No. 0.94;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLGHPVCDs 10
Db 132 NLGHSVCDs 141

RESULT 5
S48779
L1 protein - human papillomavirus (isolate vs102-4) (fragment)
N:Alternate names: capsid protein L1
C:Species: human papillomavirus
A:Variety: isolate vs102-4
C:Date: 10-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 26-Aug-1999
R:Shamanin, V.; Glover, M.; Rausch, C.; Proby, C.; Leigh, I.M.; zur Hausen, H.; Villie
submitted to the EMBL Data Library, June 1994
A:Description: Specific types of HPV found in benign proliferations and carcinomas of
A:Reference number: S48779
A:Accession: S48779
A:Molecule type: DNA
A:Residues: 1-224 <SHA>
A:Cross-references: EMBL:X79946; NID:q562310; PDB:CAA56234.1; PDB:q562311
A:Experimental source: isolate vs102-4
C:Superfamily: papillomavirus L1 protein
C:Keywords: late protein

Query Match      69.5%; Score 41; DB 2; Length 224;
Best Local Similarity 69.2%; Pred. No. 4.7;
Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 2 LGEH----PVCDS 10
Db 57 LGEHWDKAPVCDs 69

RESULT 6
T16235
hypothetical protein F32A5.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16235
R:Pauley, A.
submitted to the EMBL Data Library, July 1995
A:Description: The sequence of C. elegans cosmid F32A5.
A:Reference number: Z18482
A:Accession: T16235
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-925 <PAU>
A:Cross-references: EMBL:U40864; NID:q669026; PDB:q669027; PDB:AA46640.1; CESP:F32A
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:F32A5.1
A:Introns: 36/3; 142/1, 172/2, 263/3; 349/1, 521/1, 595/1, 772/2, 812/1

Query Match      66.1%; Score 39; DB 2; Length 925;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GEHPVC 8
Db 6 GEHPVC 11

RESULT 7
T15348
hypothetical protein B0350.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T15348
R:Gattung, S.

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Oct 23 14:06:17 2002

submitted to the EMBL Data Library, February 1996  
 A:Description: The sequence of *C. elegans* cosmid B0350.  
 A:Reference number: Z18332  
 A:Accession: T15348  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-5170 <GAT>  
 A:Cross-references: EMBL:U50071; NID:g1208871; PID:g1208877; PIDN:AAA93447.1; CESP:B0350  
 C:Genetics:  
 A:Gene: CESP:B0350.1  
 A:Introns: 48/1; 5039/3; 5116/3

Query Match 66.1%; Score 39; DB 2; Length 5170;  
 Best Local Similarity 85.7%; Pred. No. 2; 6e+02; Indels 0; Gaps 0;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 EHPVCS 10  
 ||| |||  
 Db 572 EHPACDS 578

RESULT 8  
 C81903  
 hypothetical protein NMA1343 [imported] - *Neisseria meningitidis* (strain Z2491 serogroup  
 C:Species: *Neisseria meningitidis*  
 C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
 C:Accession: C81903  
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
 C:Accession: C81903  
 A:Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.  
 A:Reference number: A81775; MUID:20222556  
 A:Accession: C81903  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-186 <PAR>  
 A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84591.1; PID:g738001  
 A:Experimental source: serogroup A, strain Z2491  
 C:Genetics:  
 A:Gene: NMA1343

Query Match 64.4%; Score 38; DB 2; Length 186;  
 Best Local Similarity 75.0%; Pred. No. 14; Indels 1; Gaps 0;  
 Matches 6; Conservative 1; Mismatches 0; Gaps 0;

QY 1 NLGHPVC 8  
 ||| |||  
 Db 98 NLEHPMC 105

RESULT 9  
 D81118  
 conserved hypothetical protein / ankyrin-related protein NMB1133, NMB1171 [imported] - *N*  
 C:Species: *Neisseria meningitidis*  
 C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
 C:Accession: D81118; A81114  
 R:Tellet, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.  
 Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
 ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizzia, M.  
 Science 287, 1809-1815, 2000  
 A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve  
 A:Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.  
 A:Reference number: A81000; MUID:20175755  
 A:Accession: D81118  
 A:Molecule type: DNA  
 A:Residues: 1-253 <TET>  
 A:Cross-references: GB:AE002098; NID:g7226363; PIDN:AAF41521.1; PID:g722637  
 A:Experimental source: serogroup B, strain MC58  
 A:Accession: A81114  
 A:Molecule type: DNA  
 A:Residues: 1-253 <TET>  
 A:Cross-references: GB:AE002465; GB:AE002098; NID:g7226401; PIDN:AAF41556.1; PID:g722640  
 A:Experimental source: serogroup B, strain MC58

C:Genetics:  
 A:Gene: NMB1133; NMB1171

Query Match 64.4%; Score 38; DB 2; Length 253;  
 Best Local Similarity 75.0%; Pred. No. 19;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLGHPVC 8  
 ||| |||  
 Db 165 NLEHPMC 172

RESULT 10

T20741  
 hypothetical protein F11A3.1 - *Caenorhabditis elegans*  
 C:Species: *Caenorhabditis elegans*  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Aug-2000  
 C:Accession: T20741  
 R:McMurry, A.  
 submitted to the EMBL Data Library, April 1996  
 A:Reference number: Z19318  
 A:Accession: T20741  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-544 <WIL>  
 A:Cross-references: EMBL:Z70751; PIDN:CAA94751.1; GSPDB:GN00023; CESP:F11A3.1  
 A:Experimental source: clone F11A3  
 C:Genetics:  
 A:Gene: CESP:F11A3.1  
 A:Map position: 5  
 A:Introns: 70/3, 108/1, 217/2, 282/3; 375/4, 505/1  
 C:Superfamily: 4-coumarate-CoA ligase; acetate-CoA ligase homology  
 F:67-536/Domain: acetate-CoA ligase homology <ACL>

Query Match 64.4%; Score 38; DB 2; Length 544;  
 Best Local Similarity 62.5%; Pred. No. 41;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LGEHPVCD 9  
 ||| |||  
 Db 296 LAKHPICD 303

RESULT 11

JC7620  
 guanylin precursor, long form - European eel  
 C:Species: *Anguilla anguilla* (European eel)  
 C:Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 03-Aug-2001  
 C:Accession: JC7620  
 R:Comrie, M.M.; Cutler, C.P.; Gramb, G.  
 Biochem. Biophys. Res. Commun. 281, 1078-1085, 2001  
 A:Title: Cloning and expression of guanylin from the European eel (*Anguilla anguilla*)  
 A:Reference number: JC7620; MUID:21139737; PMID:11243845  
 A:Accession: JC7620  
 A:Molecule type: mRNA  
 A:Residues: 1-116 <COM>  
 A:Cross-references: GB:AJ301673  
 C:Comment: This protein, a member of a family of heat-stable peptides, is a potent ex  
 axis. This peptide signalling system plays a role in osmoregulation in euryhaline te  
 C:Superfamily: guanylin  
 C:Keywords: heat-stable protein; osmoregulation  
 F:1-28/Domain: signal sequence #status predicted <SIG>  
 F:29-116/Product: guanylin precursor, long form #status predicted <MAT>  
 F:33-39/Region: homologous #status predicted  
 F:69-114/Region: highly conserved #status predicted

Query Match 62.7%; Score 37; DB 2; Length 116;  
 Best Local Similarity 60.0%; Pred. No. 13;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NLGHPVCS 10  
 ||| |||  
 Db 62 NLGSHAVCSN 71

us-09-613-355d-3\_l.rpr

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C:Superfamily: nerve growth factor beta chain

Query Match 61.0%; Score 36; DB 2; Length 117;  
 Best Local Similarity 70.0%; Pred. No. 20;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NLGHPVCD 10  
 Db 5 NOGFSVCD 14

RESULT 15

S48451

Probable membrane protein YIL006w - yeast (Saccharomyces cerevisiae)

C:Species: Saccharomyces cerevisiae

C:Date: 02-Dec-1994 #sequence\_revision 02-Dec-1994 #text\_change 31-Mar-2000

C:Accession: S48451

R:Rowley, N.

submitted to the EMBL Data Library, August 1994

A:Reference number: S48442

A:Accession: S48451

A:Molecule type: DNA

A:Residues: 1-373 &lt;POW&gt;

A:Cross-references: GB:247047, EMBL:238113, NID:3623937, PID:3763340; MIPS:YIL006w

C:Genetics:

A:Map position: 9L

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

C:Keywords: duplication; mitochondrion; transmembrane protein

F:74-167/Domain: ADP,ATP carrier protein repeat homology &lt;ACP1&gt;

F:79-95/Domain: transmembrane #status predicted &lt;TM1&gt;

F:173-264/Domain: ADP,ATP carrier protein repeat homology &lt;ACP2&gt;

F:236-252/Domain: transmembrane #status predicted &lt;TM2&gt;

F:275-365/Domain: ADP,ATP carrier protein repeat homology &lt;ACP3&gt;

Query Match 61.0%; Score 36; DB 2; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 65;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGHP 6  
 Db 209 NLGHP 214

Search completed: October 23, 2002, 12:16:00

Job time : 18 secs

RESULT 12

S51320

Mitogen-activated protein kinase 6 (EC 2.7.1.1) - common tobacco

N:Alternate names: serine/threonine-specific protein kinase p43Ntif6

C:Species: Nicotiana tabacum (common tobacco)

C:Date: 07-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 18-Jun-1999

C:Accession: S68189, S51320

R:Wilson, C.; Anglimayer, K.; Vicente, O.; Heberle-Bors, E.

Eur. J. Biochem. 233, 249-257, 1995

A:Title: Molecular cloning, functional expression in Escherichia coli, and characterization

A:Reference number: S68189; MUID:96061956

A:Accession: S68189

A:Molecule type: mRNA

A:Residues: 1-371 &lt;WL2&gt;

A:Cross-references: EMBL:X83879, NID:3634067, FIDH:CAA58760.1; PID:3634068

C:Genetics:

A:Gene: ntf6

C:Superfamily: kinase-related transforming protein; protein kinase homology

C:Keywords: Atg; phosphotransferase; serine/threonine-specific protein kinase

F:35-324/Domain: protein kinase homology &lt;KIN&gt;

F:44-52/Region: protein kinase ATP-binding motif

Query Match 62.7%; Score 37; DB 2; Length 371;  
 Best Local Similarity 66.7%; Pred. No. 42;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LGHPVCD 10  
 Db 330 INEPVCD 338

RESULT 13

B41950

retrovirus-related hypothetical protein 2 - Trypanosoma cruzi retrotransposon

C:Species: Trypanosoma cruzi

C:Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 08-Jan-1999

C:Accession: B41950

R:Villanueva, M.S.; Williams, S.P.; Beard, C.B.; Richards, F.F.; Aksoy, S.

Mol. Cell. Biol. 11, 6139-6148, 1991

A:Title: A new member of a family of site-specific retrotransposons is present in the sp

A:Reference number: A41950; MUID:92049344

A:Accession: B41950

A&gt;Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1317 &lt;VIL&gt;

A:Cross-references: GB:M62862, NID:3162247; PID:3162249

A:Note: sequence extracted from NCBI backbone (NCBI:66378, NCBIP:66380)

Query Match 62.7%; Score 37; DB 2; Length 1317;  
 Best Local Similarity 71.4%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GEHPVCD 9  
 Db 30 GGPICD 36

RESULT 14

S28161

nerve growth factor beta chain - Russell's viper

C:Species: Vipera russelli (Russell's viper)

C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997

C:Accession: S28161

R:Koyama, J.; Inoue, S.; Ikeda, K.; Hayashi, K.

Biochim. Biophys. Acta 1160, 287-292, 1992

A:Title: Purification and amino-acid sequence of a nerve growth factor from the venom of

A:Reference number: S28161; MUID:93120151

A:Accession: S28161

A&gt;Status: preliminary

A:Molecule type: protein

A:Residues: 1-117 &lt;KOY&gt;

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Arabisopsis thalia  
Arabisopsis thalia  
Novel human diago  
Novel human diago  
Human polypeptide  
Propionibacterium  
Human polypeptide  
Human CARD-6 prote  
Human polypeptide  
Human protein sequ  
Novel signal trans  
Novel human neopla  
Human protein sequ  
Human G protein as  
Mutant huNT-3 1-11  
Human NT-3(1-117)R  
Chimeric neurotrop  
NGF, mouse, Mus m  
Mutant met-huNT-3  
Human r-methuNT-3  
NT-3, mouse, Mus  
Neurotrophin-3, R  
Human neurotrophin  
Mutant huNT-3 1-11  
Neurotrophin-3 will  
Human neurotrophin-3  
Human neurotrophin  
Human NT-3(1-115)R  
Nerve growth facto  
NT-3 amino acid se  
Chimeric neurotrop  
Chimeric neurotrop  
Chimeric neurotrop

12 36 61.0 118 21 AAG11707  
13 36 61.0 130 21 AAG11706  
14 36 61.0 180 22 ABC08318  
15 36 61.0 213 22 ABG14503  
16 36 61.0 222 22 AAO11203  
17 36 61.0 326 22 AAU41494  
18 36 61.0 596 22 AAG64029  
19 36 61.0 1037 22 AAB20087  
20 35.5 60.2 108 22 AAC04935  
21 35.5 60.2 359 22 AAB93279  
22 35.5 60.2 386 22 AAU17446  
23 35.5 60.2 386 22 AAU21629  
24 35.5 60.2 798 22 AAB94519  
25 35.5 60.2 914 22 AAB82972  
26 35 59.3 117 19 AAW52303  
27 35 59.3 117 19 AAE05872  
28 35 59.3 118 13 AAR21874  
29 35 59.3 118 13 AAR29493  
30 35 59.3 118 19 AAW52301  
31 35 59.3 118 22 AAE05870  
32 35 59.3 119 13 AAR29495  
33 35 59.3 119 15 AAR54086  
34 35 59.3 119 19 AAW48889  
35 35 59.3 119 19 AAW52302  
36 35 59.3 119 20 AAW81118  
37 35 59.3 119 21 AAB29113  
38 35 59.3 119 21 AAY92008  
39 35 59.3 119 22 AAE05871  
40 35 59.3 119 22 AAG64595  
41 35 59.3 119 22 AAB35946  
42 35 59.3 120 13 AAR21866  
43 35 59.3 120 13 AAR21867  
44 35 59.3 120 13 AAR21868  
45 35 59.3 120 13 AAR21869

# ALIGNMENTS

RESULT 1  
AAM89511  
ID AAM89511 standard; Protein; 73 AA.  
AC AAM89511;  
XX  
XX  
DT 07-NOV-2001 (first entry)  
XX Human immune/haematopoietic antigen SEQ ID NO:17104.  
DE  
DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
KW cytotaxtic; gene therapy; vaccine; metastasis.  
XX  
XX Homo sapiens.  
OS  
PN WO200157182-A2.  
XX  
PD 09-AUG-2001  
XX  
XX 17-JAN-2001; 2001WO-US01354.  
XX  
XX 31-JAN-2000; 2000US-0179065.  
FR 04-FEB-2000; 2000US-0180628.  
FR 24-FEB-2000; 2000US-0184664.  
FR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
PR 07-JUL-2000; 2000US-0216880.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No	Score	Query Match	length	ID	Description
1	43	72.9	73	AAM89511	Human immune/haemia
2	43	72.9	889	22 AAB66958	Drosophila melanog
3	41	69.5	224	16 AAR88274	Papilloma virus ma
4	40	67.8	404	17 AAR97833	Kaposi's sarcoma a
5	40	67.8	404	17 AAR93609	Kaposi's sarcoma a
6	39	66.1	60	22 AAM87222	Human immune/haemia
7	39	66.1	74	22 AAU48620	Propionibacterium
8	38	64.4	79	22 AAU60325	Propionibacterium
9	38	64.4	87	22 AAO08031	Human polypeptide
10	38	64.4	105	22 AAU54570	Propionibacterium
11	38	64.4	1529	21 AAY96744	A. terreus ORF1 es

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 23, 2002, 12 10 29 : Search time 31 Seconds  
(without alignments)  
35.830 Million cell updates/sec

Title: US-09-613-355D-3

Perfect score: 59  
Sequence: 1 NLGHPVCD5 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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wo 01/5-7-182  
cargen  
Pub-8-9-07

us-09-613-355d-3\_1.rag

Wed Oct 23 14:06:12 2002

PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
PR 26-JUL-2000; 2000US-0220964.  
PR 14-AUG-2000; 2000US-0224418.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
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PR 18-AUG-2000; 2000US-0226681.  
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PR 22-AUG-2000; 2000US-0227182.  
PR 22-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0229487.  
PR 01-SEP-2000; 2000US-0229344.  
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PR 01-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229514.  
PR 05-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.  
PR 08-SEP-2000; 2000US-0231242.  
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PR 12-SEP-2000; 2000US-0231968.  
PR 14-SEP-2000; 2000US-0232397.  
PR 14-SEP-2000; 2000US-0232398.  
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PR 14-SEP-2000; 2000US-0232401.  
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PR 14-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-0234223.  
PR 21-SEP-2000; 2000US-0234274.  
PR 25-SEP-2000; 2000US-0234997.  
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PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
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PR 29-SEP-2000; 2000US-0236369.  
PR 29-SEP-2000; 2000US-0236370.  
PR 29-SEP-2000; 2000US-0236802.  
PR 02-OCT-2000; 2000US-0237037.  
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PR 08-NOV-2000; 2000US-0246474.  
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PR 17-NOV-2000; 2000US-0249244.  
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PR 01-DEC-2000; 2000US-0250160.  
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PR 06-DEC-2000; 2000US-0251479.  
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PR 08-DEC-2000; 2000US-0251868.  
PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251989.  
PR 08-DEC-2000; 2000US-0251990.  
PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.  
Rosen CA, Barash SC, Ruben SM;  
WPI, 2001-483426/52  
N-PSDB; AAK62292.  
Nucleic acids encoding human immune/hematopoietic antigen polypeptides,  
useful for preventing, diagnosing and/or treating cancers and  
metastasis.  
Claim 11; SEQ ID NO 17104; 3071pp + Sequence Listing: English.  
AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)  
amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic  
activity, and can be used in gene therapy and vaccine production. (I)  
proteins and polynucleotides may be used in the prevention, diagnosis and  
treatment of diseases associated with inappropriate (I) expression. For  
example, they may be used to treat disorders associated with decreased  
expression by rectifying mutations or deletions in a patient's genome  
that affect the activity of (I) by expressing inactive proteins or to  
supplement the patients own production of (I). Additionally, (I)

CC polynucleotides may be used to produce the secreted (I), by inserting the  
CC the nucleic acids into a host cell and culturing the cell to express the  
CC protein. (I) proteins and polynucleotides may be used to prevent,  
CC diagnose and treat immune/haematopoietic-related diseases, especially  
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703  
CC to AAK87694 represent human immune/haematopoietic antigen genomic  
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169  
CC represent sequences used in the exemplification of the present invention.  
XX  
SQ Sequence 73 AA;

Query Match 72.9%; Score 43; DB 22; Length 73;  
Best Local Similarity 75.0%; Pred. No. 3.3;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 2 LGEHPVCD 9  
DB 40 LGQHPLCD 47  
II:II:II

RESULT 2  
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ID ABB6958 standard; Protein: 889 AA.  
XX  
AC ABB6958;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Drosophila melanogaster polypeptide SEQ ID NO 27666.  
XX  
KW Drosophila; developmental biology; cell signalling; insecticide;  
KW pharmaceutical.  
XX  
OS Drosophila melanogaster.  
XX  
PN WO200171042-A2.  
XX  
PD 27-SEP-2001.  
XX  
PF 23-MAR-2001; 2001WO-US09231.  
XX  
PP 23-MAR-2000; 2000US-141537P.  
PR 11-JUL-2000; 2000US-0614150.  
XX  
PA (PEKE ) PE CORP NY.  
XX  
PI Venter JC, Adams M, Li PWD, Myers EW;  
XX  
DR WPI: 2001-656860/75.  
XX  
N-PSDB: ABL11061.

XX New isolated nucleic acid detection reagent for detecting 1000 or more  
XX genes from Drosophila and for elucidating cell signalling and cell-cell  
XX interactions -  
XX Disclosure; SEQ ID NO 27666; 21pp + Sequence Listing; English.  
XX  
XX The invention relates to an isolated nucleic acid detection reagent  
XX capable of detecting 1000 or more genes from Drosophila. The invention is  
XX useful in developmental biology and in elucidating cell signalling and  
XX cell-cell interactions in higher eukaryotes for the development of  
XX insecticides, therapeutics and pharmaceutical drugs. The invention  
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
XX sequences (ABL01840-ABL16175) and the encoded proteins  
XX (ABB57737-ABB72072).  
XX The sequence data for this patent did not form part of the printed  
XX specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 889 AA;  
XX  
XX Query Match 72.9%; Score 43; DB 22; Length 889;  
XX Best Local Similarity 100.0%; Pred. No. 41;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 LGEHPVCD 8  
DB 309 LGEHPVCD 315  
II:II:II

RESULT 3  
AAR88274  
ID AAR88274 standard; Peptide: 224 AA.  
XX  
AC AAR88274;  
XX  
DT 12-JUN-1996 (first entry)  
XX  
DE Papilloma virus major capsid protein.  
XX  
KW HP-Virus 15; papilloma virus; major;  
KW capsid protein; plasmid VS92.1; DSM 9140; diagnosis;  
KW skin carcinomas; therapy; vaccination.  
XX  
OS Papilloma virus.  
XX  
PN DE4415743-A1.  
XX  
PD 09-NOV-1995.  
XX  
PF 04-MAY-1994; 94DE-4415743.  
XX  
PR 04-MAY-1994; 94DE-4415743.  
XX  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
XX  
PI de Villiers zur Hausen E, Leigh I, Shamanin V, zur Hausen H;  
XX  
DR WPI: 1995-383680/50.  
XX  
N-PSDB: AAT03506.  
XX  
PT DNA encoding peptide(s) of papilloma virus major capsid protein -  
XX useful for detecting papilloma virus in skin carcinoma  
XX  
XX Claim 7; Fig 8; 15pp; German.  
XX  
XX AAT03506 is 82.8% homologous to HP-Virus 15, encodes AAR88274 a  
XX peptide of papilloma virus (PV) major capsid protein and is  
XX expressed by the plasmid VS92-1 (DSM 9140). The DNA is useful  
XX in diagnosis, esp. to detect PV in skin carcinomas. Major capsid  
XX proteins encoded by a PV genome contg. the DNA are useful for  
XX therapy and/or vaccination.  
XX  
SQ Sequence 224 AA;

Query Match 69.5%; Score 41; DB 16; Length 224;  
Best Local Similarity 69.2%; Pred. No. 23;  
Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;  
QY 2 LGEH----PVCD 10  
DB 57 LGEHWDKAPVCD 69  
II:II:II

RESULT 4  
AAR97833  
ID AAR97833 standard; Protein: 404 AA.  
XX  
AC AAR97833;  
XX  
DT 11-SEP-1996 (first entry)  
XX  
DE Kaposi's sarcoma associated herpesvirus ORF23 product.  
XX  
KW Kaposi's sarcoma, gamma-2 herpesvirus; KSHV; therapy; diagnosis;  
XX vaccine; diagnosis; AIDS.

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XX OS Kaposi's sarcoma associated herpesvirus.

XX PN WO9615779-A1.

XX PD 30-MAY-1996.

XX PF 21-NOV-1995; 95WO-US15138.

XX PR 11-APR-1995; 95US-0420235.

XX PA (UYCO ) UNIV COLUMBIA NEW YORK.

XX PI Chang Y, Moore PS;

XX PN N-PSDB; AAT30685.

XX DR Herpes virus associated with Kaposi's sarcoma - also definitive DNA

XX PT sequences, useful for diagnosis of and to develop prods. for

XX PT treatment of Kaposi's sarcoma

XX PS Claim 17; Page 203-205; 277pp; English.

XX SQ Lambda clone KS5 (AAT30681) is a fragment of a newly identified human

XX CC gamma-2 herpesvirus associated with Kaposi's sarcoma (KS). KS5 has

XX CC 17 open reading frames (AAT30682-98), 15 of which are complete,

XX CC including ORF23 (AAT30685). The protein products (AAR97830-46,

XX CC respectively) of the 17 ORFs can be expressed in eukaryotic or

XX CC bacterial host cells for use as vaccines, for KS diagnosis, or for

XX SQ raising antibodies.

XX SQ Sequence 404 AA;

XX Query Match 67.8%; Score 40; DB 17; Length 404;

XX Best Local Similarity 87.5%; Pred. No. 61;

XX Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX QY 2 LGHEPVCDC 9

XX DB 225 LGESPVCDC 232

XX RESULT 5

XX ID AAR93609 standard; Protein: 404 AA.

XX AC AAR93609;

XX DT 13-AUG-1996 (first entry)

XX DE Kaposi's sarcoma associated herpesvirus ORF23 product.

XX KW Kaposi's sarcoma; KSHV; lymphoma; AIDS; vaccine; diagnosis;

XX KW therapy.

XX OS Kaposi's sarcoma associated herpesvirus.

XX PN WO9606159-A1.

XX PD 29-FEB-1996.

XX PF 11-AUG-1995; 95WO-US10194.

XX PR 11-APR-1995; 95US-0420235.

XX PA 18-AUG-1994; 94US-0292365.

XX PA 21-NOV-1994; 94US-0343100.

XX PA (UYCO ) UNIV COLUMBIA NEW YORK

XX PA (GRAN/) GRANT D E.

XX PA (VIEL/) VIELE L.

PI Chang Y, Moore PS, Grant DE, Viele L;

XX DR WPI: 1996-151362/15.

XX N-PSDB; AAT16815.

XX PT Herpes-virus DNA associated with Kaposi's sarcoma - also associated

XX PT vectors and proteins, used in detection and vaccination.

XX PS Claim 17; Page 216-218; 305pp; English.

XX SQ Kaposi's sarcoma associated herpes virus (KSHV) clone KS5 (AAT16806),

XX CC obt'd. from a KS lesion genomic library, includes 15 complete ORFs and

XX CC 2 incomplete ORFs (AAT16807-23) named according to their Herpesvirus

XX CC salmuri positional homologues. The ORF23 (AAT16815) product is

XX CC given in AAR93609. KSHV proteins and peptides may be obt'd. by

XX CC incorporating encoding sequences into a vector and expression in

XX CC host cells. They are useful in vaccines or for raising antibodies of

XX CC diagnostic or therapeutic value.

XX SQ Sequence 404 AA;

XX Query Match 67.8%; Score 40; DB 17; Length 404;

XX Best Local Similarity 87.5%; Pred. No. 61;

XX Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX QY 2 LGHEPVCDC 9

XX DB 225 LGESPVCDC 232

XX RESULT 6

XX ID AAM87222 standard; Protein: 60 AA.

XX AC AAM87222;

XX DT 07-NOV-2001 (first entry)

XX DE Human immune/haematopoietic antigen SEQ ID NO:14815.

XX KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;

XX KW cytostatic; gene therapy; vaccine; metastasis.

XX OS Homo sapiens.

XX PN WO200157182-A2.

XX PD 09-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US01354.

XX PR 31-JAN-2000; 2000US-0179065.

XX PR 04-FEB-2000; 2000US-0180628.

XX PR 24-FEB-2000; 2000US-0184564.

XX PR 02-MAR-2000; 2000US-0186350.

XX PR 16-MAR-2000; 2000US-0189874.

XX PR 17-MAR-2000; 2000US-0190076.

XX PR 18-APR-2000; 2000US-0198123.

XX PR 19-MAY-2000; 2000US-0205515.

XX PR 07-JUN-2000; 2000US-0209467.

XX PR 28-JUN-2000; 2000US-0214886.

XX PR 30-JUN-2000; 2000US-0215135.

XX PR 07-JUL-2000; 2000US-0216647.

XX PR 07-JUL-2000; 2000US-0216880.

XX PR 11-JUL-2000; 2000US-0217487.

XX PR 11-JUL-2000; 2000US-0218290.

XX PR 14-JUL-2000; 2000US-0220963.

XX PR 26-JUL-2000; 2000US-0220964.

XX PR 14-AUG-2000; 2000US-0224518.

XX PR 14-AUG-2000; 2000US-0225213.

XX PR 14-AUG-2000; 2000US-0225214.



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PR 14-AUG-2000; 2000US-0225266.  
 PR 14-AUG-2000; 2000US-0225267.  
 PR 14-AUG-2000; 2000US-0225268.  
 PR 14-AUG-2000; 2000US-0225270.  
 PR 14-AUG-2000; 2000US-0225447.  
 PR 14-AUG-2000; 2000US-0225757.  
 PR 14-AUG-2000; 2000US-0225758.  
 PR 14-AUG-2000; 2000US-0225759.  
 PR 18-AUG-2000; 2000US-0226279.  
 PR 22-AUG-2000; 2000US-0226681.  
 PR 22-AUG-2000; 2000US-0226868.  
 PR 22-AUG-2000; 2000US-0227182.  
 PR 23-AUG-2000; 2000US-0227009.  
 PR 30-AUG-2000; 2000US-0228924.  
 PR 01-SEP-2000; 2000US-0229287.  
 PR 01-SEP-2000; 2000US-0229343.  
 PR 01-SEP-2000; 2000US-0229344.  
 PR 01-SEP-2000; 2000US-0229345.  
 PR 05-SEP-2000; 2000US-0229509.  
 PR 05-SEP-2000; 2000US-0229513.  
 PR 06-SEP-2000; 2000US-0230437.  
 PR 06-SEP-2000; 2000US-0230438.  
 PR 08-SEP-2000; 2000US-0231242.  
 PR 08-SEP-2000; 2000US-0231243.  
 PR 08-SEP-2000; 2000US-0231244.  
 PR 08-SEP-2000; 2000US-0231411.  
 PR 08-SEP-2000; 2000US-0231414.  
 PR 08-SEP-2000; 2000US-0232080.  
 PR 08-SEP-2000; 2000US-0232081.  
 PR 12-SEP-2000; 2000US-0231968.  
 PR 14-SEP-2000; 2000US-0232397.  
 PR 14-SEP-2000; 2000US-0232398.  
 PR 14-SEP-2000; 2000US-0242399.  
 PR 14-SEP-2000; 2000US-0232400.  
 PR 14-SEP-2000; 2000US-0232401.  
 PR 14-SEP-2000; 2000US-0233063.  
 PR 14-SEP-2000; 2000US-0233064.  
 PR 14-SEP-2000; 2000US-0233065.  
 PR 21-SEP-2000; 2000US-0234223.  
 PR 21-SEP-2000; 2000US-0234274.  
 PR 25-SEP-2000; 2000US-0234997.  
 PR 25-SEP-2000; 2000US-0234998.  
 PR 26-SEP-2000; 2000US-0235484.  
 PR 27-SEP-2000; 2000US-0235834.  
 PR 27-SEP-2000; 2000US-0235836.  
 PR 29-SEP-2000; 2000US-0236327.  
 PR 29-SEP-2000; 2000US-0236367.  
 PR 29-SEP-2000; 2000US-0236368.  
 PR 29-SEP-2000; 2000US-0236369.  
 PR 29-SEP-2000; 2000US-0236370.  
 PR 02-OCT-2000; 2000US-0236802.  
 PR 02-OCT-2000; 2000US-0237037.  
 PR 02-OCT-2000; 2000US-0237038.  
 PR 02-OCT-2000; 2000US-0237039.  
 PR 02-OCT-2000; 2000US-0237040.  
 PR 13-OCT-2000; 2000US-0239935.  
 PR 13-OCT-2000; 2000US-0239937.  
 PR 20-OCT-2000; 2000US-0240460.  
 PR 20-OCT-2000; 2000US-0241221.  
 PR 20-OCT-2000; 2000US-0241785.  
 PR 20-OCT-2000; 2000US-0241786.  
 PR 20-OCT-2000; 2000US-0241787.  
 PR 20-OCT-2000; 2000US-0241808.  
 PR 20-OCT-2000; 2000US-0241809.  
 PR 20-OCT-2000; 2000US-0241826.  
 PR 01-NOV-2000; 2000US-0244617.  
 PR 08-NOV-2000; 2000US-0246474.  
 PR 08-NOV-2000; 2000US-0246475.  
 PR 08-NOV-2000; 2000US-0246476.  
 PR 08-NOV-2000; 2000US-0246477.  
 PR 08-NOV-2000; 2000US-0246478.  
 PR 08-NOV-2000; 2000US-0246523.  
 PR 08-NOV-2000; 2000US-0246524.

PR 08-NOV-2000; 2000US-0246525.  
 PR 08-NOV-2000; 2000US-0246526.  
 PR 08-NOV-2000; 2000US-0246527.  
 PR 08-NOV-2000; 2000US-0246528.  
 PR 08-NOV-2000; 2000US-0246532.  
 PR 08-NOV-2000; 2000US-0246609.  
 PR 08-NOV-2000; 2000US-0246610.  
 PR 08-NOV-2000; 2000US-0246611.  
 PR 08-NOV-2000; 2000US-0246613.  
 PR 17-NOV-2000; 2000US-0249297.  
 PR 17-NOV-2000; 2000US-0249208.  
 PR 17-NOV-2000; 2000US-0249209.  
 PR 17-NOV-2000; 2000US-0249210.  
 PR 17-NOV-2000; 2000US-0249211.  
 PR 17-NOV-2000; 2000US-0249212.  
 PR 17-NOV-2000; 2000US-0249213.  
 PR 17-NOV-2000; 2000US-0249214.  
 PR 17-NOV-2000; 2000US-0249215.  
 PR 17-NOV-2000; 2000US-0249216.  
 PR 17-NOV-2000; 2000US-0249217.  
 PR 17-NOV-2000; 2000US-0249218.  
 PR 17-NOV-2000; 2000US-0249244.  
 PR 17-NOV-2000; 2000US-0249245.  
 PR 17-NOV-2000; 2000US-0249264.  
 PR 17-NOV-2000; 2000US-0249265.  
 PR 17-NOV-2000; 2000US-0249297.  
 PR 17-NOV-2000; 2000US-0249299.  
 PR 17-NOV-2000; 2000US-0249300.  
 PR 01-DEC-2000; 2000US-0250160.  
 PR 01-DEC-2000; 2000US-0250391.  
 PR 05-DEC-2000; 2000US-0251030.  
 PR 05-DEC-2000; 2000US-0251988.  
 PR 05-DEC-2000; 2000US-0256719.  
 PR 06-DEC-2000; 2000US-0253479.  
 PR 08-DEC-2000; 2000US-0251856.  
 PR 08-DEC-2000; 2000US-0251868.  
 PR 08-DEC-2000; 2000US-0251869.  
 PR 08-DEC-2000; 2000US-0251989.  
 PR 08-DEC-2000; 2000US-0251990.  
 PR 11-DEC-2000; 2000US-0254097.  
 PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.  
 Rosen CA, Barash SC, Ruben SM;  
 WFL: 2001-1834-6/52.  
 N-PSDB: AAK60003.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Claim 11: SEQ ID NO 14815; 3071pp + Sequence Listing: English.

AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I) amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patient's own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/hematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/hematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAK82169 represent sequences used in the exemplification of the present invention.

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SQ Sequence 74 AA:  
 Query Match 66.1%; Score 39, DB 22; Length 74;  
 Best Local Similarity 100%; Pred. No. 16;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GEHPVC 8  
 DB 28 GEHPVC 33  
 RESULT 8  
 AAU60325  
 ID AAU60325 standard; Protein: 79 AA.  
 XX  
 AC AAU60325;  
 XX  
 DT 27-FEB-2002 (first entry)  
 XX  
 DE Propionibacterium acnes immunogenic protein #21221.  
 XX  
 KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;  
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;  
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;  
 KW dermatological; osteopathic; neuroprotectant.  
 XX  
 OS Propionibacterium acnes.  
 XX  
 PN WO200181581-A2.  
 XX  
 PD 01-NOV-2001.  
 XX  
 PF 20-APR-2001; 2001WO-US12865.  
 XX  
 PR 21-APR-2000; 2000US-199047P.  
 PR 02-JUN-2000; 2000US-208841P.  
 PR 07-JUL-2000; 2000US-216747P.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;  
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;  
 XX  
 DR WPI: 2001-616774/71.  
 DR N-PSDB; AAS59609.  
 XX  
 PT Propionibacterium acnes polypeptides and nucleic acids useful for  
 PT vaccinating against and diagnosing infections, especially useful for  
 PT treating acne vulgaris -  
 XX  
 PS Example 1: SEQ ID No 21520; 1069pp; English.  
 XX  
 CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic  
 CC polypeptides. The proteins and their associated DNA sequences are used in  
 CC the treatment, prevention and diagnosis of medical conditions caused by  
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,  
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.  
 CC P. acnes is also involved in infections of bone, joints and the central  
 CC nervous system, however it is particularly involved in the inflammatory  
 CC lesions associated with acne vulgaris. A method for detecting the  
 CC presence or absence of P. acnes in a patient comprises contacting a  
 CC sample with a binding agent that binds to the proteins of the invention  
 CC and determining the amount of bound protein in the sample. The  
 CC polypeptides may be used as antigens in the production of antibodies  
 CC specific for P. acnes proteins. These antibodies can be used to  
 CC downregulate expression and activity of P. acnes polypeptides and  
 CC therefore treat P. acnes infections. The antibodies may also be used as  
 CC diagnostic agents for determining P. acnes presence, for example, by  
 CC enzyme linked immunosorbent assay (ELISA).  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

SQ Sequence 60 AA:  
 Query Match 56.1%; Score 39, DB 22; Length 60;  
 Best Local Similarity 75.0%; Pred. No. 13;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 GEHPVCDS 10  
 DB 4 GEHPVCPS 11  
 RESULT 7  
 AAU48620  
 ID AAU48620 standard; Protein: 74 AA.  
 XX  
 AC AAU48620;  
 XX  
 DT 27-FEB-2002 (first entry)  
 XX  
 DE Propionibacterium acnes immunogenic protein #9516.  
 XX  
 KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;  
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;  
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;  
 KW dermatological; osteopathic; neuroprotectant.  
 XX  
 OS Propionibacterium acnes.  
 XX  
 PN WO200181581-A2.  
 XX  
 PD 01-NOV-2001.  
 XX  
 PF 20-APR-2001; 2001WO-US12865.  
 XX  
 PR 21-APR-2000; 2000US-199047P.  
 PR 02-JUN-2000; 2000US-208841P.  
 PR 07-JUL-2000; 2000US-216747P.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;  
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;  
 XX  
 DR WPI: 2001-616774/71.  
 DR N-PSDB; AAS59543.  
 XX  
 PT Propionibacterium acnes polypeptides and nucleic acids useful for  
 PT vaccinating against and diagnosing infections, especially useful for  
 PT treating acne vulgaris -  
 XX  
 PS Example 1: SEQ ID No 9815; 1069pp; English.  
 XX  
 CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic  
 CC polypeptides. The proteins and their associated DNA sequences are used in  
 CC the treatment, prevention and diagnosis of medical conditions caused by  
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,  
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.  
 CC P. acnes is also involved in infections of bone, joints and the central  
 CC nervous system, however it is particularly involved in the inflammatory  
 CC lesions associated with acne vulgaris. A method for detecting the  
 CC presence or absence of P. acnes in a patient comprises contacting a  
 CC sample with a binding agent that binds to the proteins of the invention  
 CC and determining the amount of bound protein in the sample. The  
 CC polypeptides may be used as antigens in the production of antibodies  
 CC specific for P. acnes proteins. These antibodies can be used to  
 CC downregulate expression and activity of P. acnes polypeptides and  
 CC therefore treat P. acnes infections. The antibodies may also be used as  
 CC diagnostic agents for determining P. acnes presence, for example, by  
 CC enzyme linked immunosorbent assay (ELISA).  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.



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Db 54 NLASHPICN 62

RESULT 11  
ID AAY96744 standard; Protein: 1529 AA.

XX AC AAY96744;  
XX DT 09-OCT-2000 (first entry)  
XX DE A. terreus ORF1 esterase-like protein.  
XX KW Lovastatin; D4B segment; monacolin J; esterase-like; ORF1; anti-lipemic;  
XX KW HMG-CoA reductase inhibitor; anti-hypercholesterolaemic; anti-fungal.  
XX OS Aspergillus terreus.

XX WO200037629-A2.  
XX 29-JUN-2000.  
XX PF 13-DEC-1999; 99WO-US29583.  
XX PR 18-DEC-1998; 98US-0215694.  
XX PA (WISC ) WISCONSIN ALUMNI RES FOUND.  
XX PI Hutchinson RC, Kennedy J, Park C;  
XX WPI: 2000-442660/38.  
XX DR N-PSDB; AAA51296.

XX Increasing lovastatin or monacolin J production in an organism, for use  
XX as antihypercholesterolemic or antifungal agents, comprises  
XX transforming the organism with a D4B segment  
XX Disclosure: Page 55-59; 116pp; English.

XX The proteins shown in AAY96744-60 are encoded by 17 genes from a  
XX cluster in Aspergillus terreus (ATCC 20542), which flank the NPKS  
XX (nonaketide polyketide synthase) gene, which is known to be required for  
XX lovastatin production. The NPKS gene is contained within the context of  
XX the entire gene cluster but is not indicated here (see US744350). The  
XX genes and proteins are named "OKF" or "Lov", where "Lov" signifies genes  
XX shown to be essential for lovastatin production. The portion of the gene  
XX cluster between ORF1 and the mid-region of LovF is referred to as the  
XX "D4B segment". Increasing lovastatin, or monacolin J, production in a  
XX lovastatin-producing organism, comprises transforming the organism with  
XX a D4B segment, and expressing it (claimed). Lovastatin will also be  
XX produced in non-lovastatin producing organisms (e.g. A. nidulans) by  
XX transformation with the D4B segment and the entire LovF gene. The  
XX methods are used to increase biosynthetic production of lovastatin (with  
XX an at least 5-fold increase) which is an anti-hypercholesterolaemic  
XX agent, and also has some anti-fungal activity. Lovastatin inhibits the  
XX conversion of hydroxymethylglutarylcoenzyme A (HMG-CoA) into mevalonate  
XX by HMG-CoA reductase. The methods can also be used to increase production  
XX of monacolin J (claimed), which has anti-fungal activity.

XX SQ Sequence 1529 AA;

Query Match 64.4%; Score 38; DB 21; Length 1529;  
Best Local Similarity 60.0%; Pred. No. 5;le+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLGHPVCDS 10  
|||:..|||

Db 1104 NLGEGICDS 1113

RESULT 12  
AAG11707  
ID AAG11707 standard; Protein: 118 AA.

XX AC AAG11707;  
XX DT 17-OCT-2000 (first entry)  
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 10527.  
XX KW Protein identification; signal transduction pathway; metabolic pathway;  
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;  
XX KW termination sequence.  
XX OS Arabidopsis thaliana.  
XX PN EPI033405-A2.  
XX PD 06-SEP-2000.  
XX PF 25-FEB-2000; 2000EP-0301439.  
XX PR 25-FEB-1999; 99US-0121825.  
XX PR 05-MAR-1999; 99US-0123180.  
XX PR 09-MAR-1999; 99US-0123548.  
XX PR 23-MAR-1999; 99US-0125788.  
XX PR 25-MAR-1999; 99US-0126264.  
XX PR 29-MAR-1999; 99US-0126785.  
XX PR 01-APR-1999; 99US-0127462.  
XX PR 08-APR-1999; 99US-0128234.  
XX PR 16-APR-1999; 99US-0129845.  
XX PR 19-APR-1999; 99US-0130077.  
XX PR 21-APR-1999; 99US-0130449.  
XX PR 23-APR-1999; 99US-0130510.  
XX PR 28-APR-1999; 99US-0130891.  
XX PR 30-APR-1999; 99US-0131449.  
XX PR 30-APR-1999; 99US-0132048.  
XX PR 04-MAY-1999; 99US-0132407.  
XX PR 05-MAY-1999; 99US-0132484.  
XX PR 06-MAY-1999; 99US-0132485.  
XX PR 07-MAY-1999; 99US-0132486.  
XX PR 11-MAY-1999; 99US-0132487.  
XX PR 14-MAY-1999; 99US-0132863.  
XX PR 14-MAY-1999; 99US-0134218.  
XX PR 14-MAY-1999; 99US-0134219.  
XX PR 14-MAY-1999; 99US-0134221.  
XX PR 14-MAY-1999; 99US-0134370.  
XX PR 18-MAY-1999; 99US-0134768.  
XX PR 19-MAY-1999; 99US-0134941.  
XX PR 20-MAY-1999; 99US-0135124.  
XX PR 21-MAY-1999; 99US-0135353.  
XX PR 24-MAY-1999; 99US-0135629.  
XX PR 25-MAY-1999; 99US-0136021.  
XX PR 27-MAY-1999; 99US-0136392.  
XX PR 28-MAY-1999; 99US-0136782.  
XX PR 01-JUN-1999; 99US-0137222.  
XX PR 03-JUN-1999; 99US-0137528.  
XX PR 04-JUN-1999; 99US-0137502.  
XX PR 07-JUN-1999; 99US-0137724.  
XX PR 08-JUN-1999; 99US-0138094.  
XX PR 10-JUN-1999; 99US-0138540.  
XX PR 14-JUN-1999; 99US-0138847.  
XX PR 16-JUN-1999; 99US-0139119.  
XX PR 16-JUN-1999; 99US-0139452.  
XX PR 17-JUN-1999; 99US-0139453.  
XX PR 17-JUN-1999; 99US-0139492.  
XX PR 18-JUN-1999; 99US-0139454.  
XX PR 18-JUN-1999; 99US-0139455.  
XX PR 18-JUN-1999; 99US-0139456.  
XX PR 18-JUN-1999; 99US-0139457.  
XX PR 18-JUN-1999; 99US-0139458.  
XX PR 18-JUN-1999; 99US-0139459.  
XX PR 18-JUN-1999; 99US-0139460.  
XX PR 18-JUN-1999; 99US-0139461.

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PR 18-JUN-1999; 99US-0139482.  
PR 18-JUN-1999; 99US-0139483.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 23-JUN-1999; 99US-0140695.  
PR 24-JUN-1999; 99US-0140823.  
PR 28-JUN-1999; 99US-0140991.  
PR 29-JUN-1999; 99US-0141287.  
PR 30-JUN-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 01-JUL-1999; 99US-0142055.  
PR 02-JUL-1999; 99US-0142390.  
PR 06-JUL-1999; 99US-0142803.  
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PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
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PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
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PR 09-AUG-1999; 99US-0147493.  
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PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
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PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
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PR 20-AUG-1999; 99US-0149723.  
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PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.

PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151330.  
PR 01-SEP-1999; 99US-0151348.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 24-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156596.  
PR 29-SEP-1999; 99US-0157117.  
PR 04-OCT-1999; 99US-0157753.  
PR 05-OCT-1999; 99US-0157865.  
PR 06-OCT-1999; 99US-0158029.  
PR 07-OCT-1999; 99US-0158232.  
PR 08-OCT-1999; 99US-0158369.  
PR 12-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
PR 13-OCT-1999; 99US-0159329.  
PR 14-OCT-1999; 99US-0159330.  
PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159637.  
PR 14-OCT-1999; 99US-0159638.  
PR 18-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160768.  
PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 25-OCT-1999; 99US-0161404.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 61.0%; Score 36; DB 21; Length 118;  
Best Local Similarity 77.8%; Pred No. 86;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 LGHPVCDS 10  
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Db 96 LGPEPVADS 104

RESULT 13  
AAG11706  
ID AAG11706 standard; Protein; 130 AA.

XX AAG11706;

XX 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 10526.  
DE  
XX

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Wed Oct 23 14:06:12 2002

KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hydridisation assay; genetic mapping; gene expression control; promoter;  
XX termination sequence.  
XX Arabidopsis thaliana.  
PN EPI033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-0301439.  
XX  
PR 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 29-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0128845.  
PR 19-APR-1999; 99US-0130077.  
PR 23-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 23-APR-1999; 99US-0130891.  
PR 28-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 07-MAY-1999; 99US-0132487.  
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PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134371.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
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PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
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PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 09-AUG-1999; 99US-0148171.  
PR 10-AUG-1999; 99US-0148319.  
PR 11-AUG-1999; 99US-0148341.  
PR 12-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 13-AUG-1999; 99US-0149368.  
PR 15-AUG-1999; 99US-0149175.  
PR 17-AUG-1999; 99US-0149426.  
PR 18-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.



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30-MAR-2001: 2001WO-US08631.  
 31-MAR-2000: 2000US-0540217.  
 23-AUG-2000: 2000US-0649167.  
 (HYSE-) HYSEQ INC.  
 Drmanac RT, Liu C, Tang YT:  
 WPI: 2001-639362/73.  
 N-PSDB: AAS78690.  
 New isolated polynucleotide and encoded polypeptides, useful in  
 diagnostics, forensics, gene mapping, identification of mutations  
 responsible for genetic disorders or other traits and to assess  
 biodiversity -  
 Claim 20: SEQ ID No 44862: 103pp: English.  
 The invention relates to isolated polynucleotide (I) and  
 polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 mapping and gene mapping, and in recombinant production of (II). The  
 polynucleotides are also used in diagnostics as expressed sequence tags  
 for identifying expressed genes. (I) is useful in gene therapy techniques  
 to restore normal activity of (II) or to treat disease states involving or  
 (II). (II) is useful for generating antibodies against it, detecting or  
 quantitating a polypeptide in tissue, as molecular weight markers and as  
 a food supplement. (II) and its binding partners are useful in medical  
 imaging of sites expressing (II). (I) and (II) are useful for treating  
 disorders involving aberrant protein expression or biological activity.  
 The polypeptide and polynucleotide sequences have applications in  
 diagnostics, forensics, gene mapping, identification of mutations  
 responsible for genetic disorders or other traits to assess biodiversity  
 and to produce other types of data and products dependent on DNA and  
 amino acid sequences. ABG00010-ABG30377 represent novel human  
 diagnostic amino acid sequences of the invention.  
 Note: The sequence data for this patent did not appear in the printed  
 specification, but was obtained in electronic format directly from WIPO  
 at ftp.wipo.int/pub/published\_pct\_sequences.  
 SQ Sequence 213 AA:  
 Query Match 61.0%; Score 36; DB 22; Length 213;  
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 EHPVCD 9  
 Db 119 QHPVCD 124  
 Search completed: October 23, 2002, 12:14:48  
 Job time : 33 secs





Wed Oct 23 14:06:03 2002

XX Disclosure; SEQ ID NO 27666; 21pp + Sequence Listing; English.

PS The invention relates to an isolated nucleic acid detection reagent

XX capable of detecting 1000 or more genes from *Drosophila*. The invention is

CC useful in developmental biology and in elucidating cell signalling and

CC cell-cell interactions in higher eukaryotes for the development of

CC insecticides, therapeutics and pharmaceutical drugs. The invention

CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA

CC sequences (ABL01840-ABL15175) and the encoded proteins

CC (ABB57737-ABB72072).

CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX

XX

SQ Sequence 889 AA:

Query Match 70.0%; Score 7, DB 22; Length 889;

Best Local Similarity 100.0%; Pred. No. 3 2;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGEHPVC 8

Db 309 LGEHPVC 315

|||||

RESULT 2

AAU56224

ID AAU56224 standard; Protein; 63 AA.

XX

AC AAU56224;

XX

XX 27-FEB-2002 (first entry)

DT

XX

DE Propionibacterium acnes immunogenic protein #17120.

XX

XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;

XX uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;

KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;

KW dermatological; osteopathic; neuroprotectant.

XX

OS Propionibacterium acnes.

XX

XX WO200181581-A2.

PN

XX

XX 01-NOV-2001.

PD

XX

XX 20-APR-2001; 2001WO-US12865.

PF

XX

XX 21-APR-2000; 2000US-199047P.

PR

XX

XX 02-JUN-2000; 2000US-208841P.

PK

XX

XX 07-JUL-2000; 2000US-216747P.

PR

XX

XX (CORI-) CORIXA CORP.

PA

XX

XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;

PI L'maisonneuve J, Zhang Y, Jen S, Carter D;

PI

XX

XX WPI: 2001-616774/71.

DR

XX

XX N-PSDB: AAS59573.

DR

XX

XX Propionibacterium acnes polypeptides and nucleic acids useful for

PT vaccinating against and diagnosing infections, especially useful for

PT treating acne vulgaris -

XX

XX Example 1: SEQ ID No 17419; 1069pp; English.

PS

XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic

XX polypeptides. The proteins and their associated DNA sequences are used in

CC the treatment, prevention and diagnosis of medical conditions caused by

CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,

CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

CC P. acnes is also involved in infections of bone, joints and the central

CC

CC nervous system, however it is particularly involved in the inflammatory

CC lesions associated with acne vulgaris. A method for detecting the

CC presence or absence of P. acnes in a patient comprises contacting a

CC sample with a binding agent that binds to the proteins of the invention

CC and determining the amount of bound protein in the sample. The

CC polypeptides may be used as antigens in the production of antibodies

CC specific for P. acnes proteins. These antibodies can be used to

CC downregulate expression and activity of P. acnes polypeptides and

CC therefore treat P. acnes infections. The antibodies may also be used as

CC diagnostic agents for determining P. acnes presence, for example, by

CC enzyme linked immunosorbent assay (ELISA).

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX

XX

SQ Sequence 63 AA:

Query Match 60.0%; Score 6, DB 22; Length 63;

Best Local Similarity 100.0%; Pred. No. 5 2;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGEHPV 7

Db 41 LGEHPV 46

|||||

RESULT 3

AAU66556

ID AAU66556 standard; Protein; 63 AA.

XX

AC AAU66556;

XX

XX 27-FEB-2002 (first entry)

DT

XX

DE Propionibacterium acnes immunogenic protein #27452.

XX

XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;

XX uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;

KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;

KW dermatological; osteopathic; neuroprotectant.

XX

OS Propionibacterium acnes.

XX

XX WO200181581-A2.

PN

XX

XX 01-NOV-2001.

PD

XX

XX 20-APR-2001; 2001WO-US12865.

PF

XX

XX 21-APR-2000; 2000US-199047P.

PR

XX

XX 02-JUN-2000; 2000US-208841P.

PK

XX

XX 07-JUL-2000; 2000US-216747P.

PR

XX

XX (CORI-) CORIXA CORP.

PA

XX

XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;

PI L'maisonneuve J, Zhang Y, Jen S, Carter D;

PI

XX

XX WPI: 2001-616774/71.

DR

XX

XX N-PSDB: AAS59741.

DR

XX

XX Propionibacterium acnes polypeptides and nucleic acids useful for

PT vaccinating against and diagnosing infections, especially useful for

PT treating acne vulgaris -

XX

XX Example 1: SEQ ID No 27751; 1069pp; English.

PS

XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic

XX polypeptides. The proteins and their associated DNA sequences are used in

CC the treatment, prevention and diagnosis of medical conditions caused by

CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,

CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

CC P. acnes is also involved in infections of bone, joints and the central

CC

nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

Query Match 60.0%; Score 6; DB 22; Length 63;  
Best Local Similarity 100.0%; Pred. No. 5.2; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0

QY 2 LGHPV 7  
DB 41 LGHPV 46  
IIIIII

RESULT 4  
AAU48620  
ID AAU48620 standard; Protein: 74 AA.  
XX AC AAU48620;  
XX DT 27-FEB-2002 (first entry)  
XX DE Propionibacterium acnes immunogenic protein #9516.  
XX KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;  
XX KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;  
XX KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;  
XX KW dermatological; osteopathic; neuroprotectant.  
XX OS Propionibacterium acnes.  
XX PN W0200181581-A2.  
XX PD 01-NOV-2001.  
XX PF 20-APR-2001; 2001WO-0512865.  
XX PR 21-APR-2000; 2000US-140047P  
XX PR 02-JUN-2000; 2000US-208841P.  
XX PR 07-JUL-2000; 2000US-216747P.  
XX PA (CORI-) CORIXA CORP.  
XX PI Skeiky YAM, Persing DH, Mitcham JL, Wang SS, Bhatia A;  
XX PI L'maisonneuve J, Zhang Y, Jen S, Carter D;  
XX WPI: 2001-616774/71.  
XX N-PSDB: AAS59543.  
XX Propionibacterium acnes polypeptides and nucleic acids useful for  
PT vaccinating against and diagnosing infections, especially useful for  
PT treating acne vulgaris -  
XX Example 1: SEQ ID No 9815; 1069pp; English.  
XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic  
XX polypeptides. The proteins and their associated DNA sequences are used in  
XX the treatment, prevention and diagnosis of medical conditions caused by  
XX P. acnes. The disorders include SAPHO syndrome (synovitis, acne,  
XX pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.  
XX P. acnes is also involved in infections of bone, joints and the central

nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

Query Match 60.0%; Score 6; DB 22; Length 74;  
Best Local Similarity 100.0%; Pred. No. 5.9; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0

QY 3 GEHPVC 8  
DB 28 GEHPVC 33  
IIIIII

RESULT 5  
ABG08318  
ID ABG08318 standard; Protein: 180 AA.  
XX AC ABG08318;  
XX DT 13-FEB-2002 (first entry)  
XX DE Novel human diagnostic protein #8309.  
XX KW Human: chromosome mapping; gene mapping; gene therapy; forensic;  
XX KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX OS Homo sapiens.  
XX PN W0200175067-A2.  
XX PD 11-OCT-2001.  
XX PF 30-MAR-2001; 2001WO-US08631.  
XX PR 31-MAR-2000; 2000US-0540217.  
XX PR 23-AUG-2000; 2000US-0649167.  
XX PA (HYSE-) HYSEQ INC  
XX PI Drmanac RT, Liu C, Tang YT;  
XX WPI: 2001-639362/73.  
XX N-PSDB: AAS72505.  
XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity -  
XX Claim 20; SEQ ID No 38677; 103pp; English.  
XX The invention relates to isolated polynucleotide (I) and  
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,  
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
XX CC and gene mapping, and in recombinant production of (II). The  
XX polynucleotides are also used in diagnostics as expressed sequence tags  
XX for identifying expressed genes. (I) is useful in gene therapy techniques  
XX to restore normal activity of (II) or to treat disease states involving  
XX (II). (II) is useful for generating antibodies against it, detecting or  
XX quantitating a polypeptide in tissue, as molecular weight markers and as

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presence or absence of *P. acnes* in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for *P. acnes* proteins. These antibodies can be used to downregulate expression and activity of *P. acnes* polypeptides and therefore treat *P. acnes* infections. The antibodies may also be used as diagnostic agents for determining *P. acnes* presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

Query Match 60.0%; Score 6; DB 22; Length 180;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGHP 6  
Db 30 NLGHP 35

RESULT 6  
AAU62691  
ID AAU62691 standard; Protein; 452 AA.

XX AC AAU62691;

XX DT 27-FEB-2002 (first entry)

XX DE Propionibacterium acnes immunogenic protein #23587.

XX KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;  
XX KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;  
XX KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;  
XX KW dermatological; osteopathic; neuroprotectant.

XX OS Propionibacterium acnes.

XX PN WO200181581-A2.

XX PD 01-NOV-2001.

XX PF 20-APR-2001; 2001WO-US12865.

XX PR 21-APR-2000; 2000US-199047P.

XX PR 02-JUN-2000; 2000US-208841P.

XX PR 07-JUL-2000; 2000US-216747P.

XX PA (CORI-) CORIXA CORP.

XX PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;

XX PI L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX XX WPI: 2001-616774/71.

XX DR N-PSDB; AAS59628.

XX PT Propionibacterium acnes polypeptides and nucleic acids useful for  
PT vaccinating against and diagnosing infections, especially useful for  
PT treating acne vulgaris -

XX PS Example 1; SEQ ID No 23886; 1069pp; English.

XX CC Sequences AAU30105-AAU68017 represent Propionibacterium acnes immunogenic  
XX CC polypeptides. The proteins and their associated DNA sequences are used in  
XX CC the treatment, prevention and diagnosis of medical conditions caused by  
XX CC *P. acnes*. The disorders include SAPHO syndrome (synovitis, acne,  
XX CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.  
XX CC *P. acnes* is also involved in infections of bone, joints and the central  
XX CC nervous system, however it is particularly involved in the inflammatory  
XX CC lesions associated with acne vulgaris. A method for detecting the

presence or absence of *P. acnes* in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for *P. acnes* proteins. These antibodies can be used to downregulate expression and activity of *P. acnes* polypeptides and therefore treat *P. acnes* infections. The antibodies may also be used as diagnostic agents for determining *P. acnes* presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

QY 2 LGHPV 7  
Db 348 LGHPV 353

RESULT 7  
AAB47444  
ID AAB47444 standard; peptide; 31 AA.

XX AC AAB47444;

XX DT 31-OCT-2001 (first entry)

XX DE Entire 3rd loop from strain nH1-1715MEE (Group 2a type).

XX KW surface exposed loop; major outer membrane protein P5; MOMP P5;  
XX KW non-typeable *H. influenzae*; nH1; LBI(f) peptide; B cell epitope;  
XX KW otitis media; sinusitis; conjunctivitis;  
XX KW lower respiratory tract infection.

XX OS Haemophilus influenzae.

XX PN WO200161013-A1.

XX PD 23-AUG-2001.

XX PF 13-FEB-2001; 2001WO-EP01556.

XX PR 15-FEB-2000; 2000GB-0003502.

XX PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX PI Berthet FJ, Denoel P, Poolman J, Thonnard J;

XX XX WPI, 2001-522599/57

XX PT Recombinant bacterial outer membrane protein where one or more  
PT surface-exposed loops are modified is useful as a vaccine to prevent or  
PT treat Haemophilus influenzae infection or associated disease, e.g.,  
PT otitis media and conjunctivitis -

XX PS Claim 2; Page 26; 29pp; English.

XX CC The sequences given in AAB47439-46 represent peptides which may be used  
XX CC to replace one or more surface exposed loops of major outer membrane  
XX CC protein P5 (MOMP P5) of non-typeable *H. influenzae* (nH1). Each of  
XX CC these peptides contain an LBI(f) peptide which is a 19 amino acid  
XX CC peptide derived from the sequence of MOMP P5 from strain nH1128,  
XX CC representing amino acids Arg17 to Gly135. This peptide represents the  
XX CC third exposed loop of P5 and is a potential B cell epitope. The loops  
XX CC of the invention are modified in terms of being in a non-native  
XX CC environment in the recombinant outer membrane protein. The modified  
XX CC MOMP P5 may be used to induce an immune response in a mammal to  
XX CC prevent or treat Haemophilus influenzae infection or associated

CC disease, e.g., otitis media, sinusitis, conjunctivitis, or lower  
CC respiratory tract infection.  
XX  
SQ Sequence 31 AA;

Query Match 50.0%; Score 5; DB 22; Length 31;  
Best Local Similarity 100.0%; Pred. No. 41;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGEH 5  
| | | | |  
Db 21 NLGEH 25

RESULT 8  
AAW14312  
ID AAW14312 standard; peptide: 34 AA.

XX AAW14312;  
XX 30-APR-1997 (first entry)

Cyclic parathyroid hormone (1-34) peptide 5.  
Cyclic parathyroid hormone fragment; calcium-regulating activity;  
osteoporosis; inhibit proliferation; epidermal cell; psoriasis;  
Improved half life; calcium retention; bone.

XX Synthetic.  
XX Key Location/Qualifiers  
XX Modified-site 13  
XX Modified-site 17

XX DE19508672-A1.  
XX 12-SEP-1996.  
XX 10-MAR-1995; 95DE-1008672.  
XX 10-MAR-1995; 95DE-1008672.

XX (BOEF ) BOEHRINGER MANNHEIM GMBH.  
XX Dony C, Esswein A, Hoffmann E, Honold K, Schaefer W;  
XX WPI; 1996-413519/42.

Cyclic parathyroid hormone fragments with lactam bridge - have good  
in vivo half life and are useful for treating osteoporosis and  
preventing epidermal cell proliferation

XX Claim 6; Page 12; 14pp; German.  
XX New cyclic parathyroid hormone fragments (CPH) have the amino acid  
sequence of h, b, p, r or CPTH(1-34), opt. extended by up to 4 amino  
acids (aa) at the C-terminus and opt. shortened by up to 3 amino acids  
at the N-terminus, and are cyclised between positions 13 and 17. One of  
these positions is occupied by L- or D- Orn or Lys, and the other by L-  
or D- Glu or Asp. CPTH have calcium-regulating activity (esp. for  
treating osteoporosis and inhibit proliferation of epidermal cells (for  
treating psoriasis). The CPTH have an improved half life in vivo than  
known PTH fragments, increased mitogenicity and DNA-synthesising  
capacity, reduced catabolic, calcium-mobilising activity and increased  
activity for calcium retention and incorporation into bone. AAW14308-16  
are claimed CPTH of the invention.

XX SQ Sequence 34 AA;  
Query Match 50.0%; Score 5; DB 17; Length 34;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGEH 5  
| | | | |  
Db 10 NLGEH 14

RESULT 9  
AAW14314  
ID AAW14314 standard; peptide: 34 AA.

XX AAW14314;  
XX 30-APR-1997 (first entry)

Cyclic parathyroid hormone (1-34) peptide 7.  
Cyclic parathyroid hormone fragment; calcium-regulating activity;  
osteoporosis; inhibit proliferation; epidermal cell; psoriasis;  
Improved half life; calcium retention; bone.

XX Synthetic.  
XX Key Location/Qualifiers  
XX Modified-site 13  
XX Modified-site 17

XX DE19508672-A1.  
XX 12-SEP-1996.  
XX 10-MAR-1995; 95DE-1008672.  
XX 10-MAR-1995; 95DE-1008672.

XX (BOEF ) BOEHRINGER MANNHEIM GMBH.  
XX Dony C, Esswein A, Hoffmann E, Honold K, Schaefer W;  
XX WPI; 1996-413519/42.  
XX Cyclic parathyroid hormone fragments with lactam bridge - have good  
in vivo half life and are useful for treating osteoporosis and  
preventing epidermal cell proliferation

CC disease, e.g., otitis media, sinusitis, conjunctivitis, or lower  
CC respiratory tract infection.  
XX  
SQ Sequence 31 AA;

Query Match 50.0%; Score 5; DB 22; Length 31;  
Best Local Similarity 100.0%; Pred. No. 41;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGEH 5  
| | | | |  
Db 21 NLGEH 25

RESULT 8  
AAW14312  
ID AAW14312 standard; peptide: 34 AA.

XX AAW14312;  
XX 30-APR-1997 (first entry)

Cyclic parathyroid hormone (1-34) peptide 5.  
Cyclic parathyroid hormone fragment; calcium-regulating activity;  
osteoporosis; inhibit proliferation; epidermal cell; psoriasis;  
Improved half life; calcium retention; bone.

XX Synthetic.  
XX Key Location/Qualifiers  
XX Modified-site 13  
XX Modified-site 17

XX DE19508672-A1.  
XX 12-SEP-1996.  
XX 10-MAR-1995; 95DE-1008672.  
XX 10-MAR-1995; 95DE-1008672.

XX (BOEF ) BOEHRINGER MANNHEIM GMBH.  
XX Dony C, Esswein A, Hoffmann E, Honold K, Schaefer W;  
XX WPI; 1996-413519/42.

Cyclic parathyroid hormone fragments with lactam bridge - have good  
in vivo half life and are useful for treating osteoporosis and  
preventing epidermal cell proliferation

XX Claim 6; Page 12; 14pp; German.  
XX New cyclic parathyroid hormone fragments (CPH) have the amino acid  
sequence of h, b, p, r or CPTH(1-34), opt. extended by up to 4 amino  
acids (aa) at the C-terminus and opt. shortened by up to 3 amino acids  
at the N-terminus, and are cyclised between positions 13 and 17. One of  
these positions is occupied by L- or D- Orn or Lys, and the other by L-  
or D- Glu or Asp. CPTH have calcium-regulating activity (esp. for  
treating osteoporosis and inhibit proliferation of epidermal cells (for  
treating psoriasis). The CPTH have an improved half life in vivo than  
known PTH fragments, increased mitogenicity and DNA-synthesising  
capacity, reduced catabolic, calcium-mobilising activity and increased  
activity for calcium retention and incorporation into bone. AAW14308-16  
are claimed CPTH of the invention.

XX SQ Sequence 34 AA;  
Query Match 50.0%; Score 5; DB 17; Length 34;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGEH 5  
| | | | |  
Db 10 NLGEH 14

RESULT 9  
AAW14314  
ID AAW14314 standard; peptide: 34 AA.

XX AAW14314;  
XX 30-APR-1997 (first entry)

Cyclic parathyroid hormone (1-34) peptide 7.  
Cyclic parathyroid hormone fragment; calcium-regulating activity;  
osteoporosis; inhibit proliferation; epidermal cell; psoriasis;  
Improved half life; calcium retention; bone.

XX Synthetic.  
XX Key Location/Qualifiers  
XX Modified-site 13  
XX Modified-site 17

XX DE19508672-A1.  
XX 12-SEP-1996.  
XX 10-MAR-1995; 95DE-1008672.  
XX 10-MAR-1995; 95DE-1008672.

XX (BOEF ) BOEHRINGER MANNHEIM GMBH.  
XX Dony C, Esswein A, Hoffmann E, Honold K, Schaefer W;  
XX WPI; 1996-413519/42.  
XX Cyclic parathyroid hormone fragments with lactam bridge - have good  
in vivo half life and are useful for treating osteoporosis and  
preventing epidermal cell proliferation

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metabolic bone disease; human; veterinary medicine;  
iontophoretic transdermal transport; recombinant E.coli.  
Synthetic.  
Key Location/Qualifiers  
Modified-site 35  
/label= "H, OTHER  
/note= "Homoserine (Hse), Hse lactone, Hse amide or  
residues 35-84 of PTH"

RESULT 10  
AAR99982  
ID AAR99982 standard; peptide: 34 AA.  
XX  
AC AAR99982;  
XX  
DT 30-APR-1997 (first entry)  
XX  
DE Canine parathyroid hormone peptide fragment (1-34).  
XX  
DE cyclic parathyroid hormone fragment; calcium-regulating activity;  
KW osteoporosis; inhibit proliferation; epidermal cell; psoriasis;  
KW improved half life; calcium retention; bone.  
XX  
OS Synthetic.  
XX  
PN DE19508672-AL.  
XX  
PD 12-SEP-1996.  
XX  
PF 10-MAR-1995; 95DE-1008672.  
XX  
PR 10-MAR-1995; 95DE-1008672.  
XX  
PA (BOEF ) BOEHRINGER MANNHEIM GMBH.  
XX  
PI Dony C, Esswein A, Hoffmann E, Honold K, Schaefer W;  
XX  
XX WPI: 1996-413519/42.  
XX  
DR Cyclic parathyroid hormone fragments with lactam bridge - have good  
XX in vivo half life and are useful for treating osteoporosis and  
PT preventing epidermal cell proliferation  
XX  
PS Disclosure; Page 10; 14pp; German.

XX New cyclic parathyroid hormone fragments (CPH) have the amino acid  
CC sequence of h, b, p, r or CPTH(1-34), opt. extended by up to 4 amino  
CC acids (aa) at the C-terminus and opt. shortened by up to 3 amino acids at  
CC the N-terminus, and are cyclised between positions 13 and 17. One of  
CC these positions is occupied by L- or D- Orn or Lys, and the other by L-  
CC or D- Glu or Asp. CPTH have calcium-regulating activity (esp. for  
CC treating osteoporosis) and inhibit proliferation of epidermal cells (for  
CC treating psoriasis). The CPTH have an improved half life in vivo than  
CC known PTH fragments, increased mitogenicity and DNA-synthesising  
CC capacity, reduced catabolic, calcium-mobilising activity and increased  
CC activity for calcium retention and incorporation into bone. The  
CC present sequence is that of canine PTH peptide fragment (1-34).  
XX  
XX  
SQ Sequence 34 AA;

Query Match 50.0%; Score 5; DB 17; Length 34;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGEH 5  
Db 10 NLGEH 14

RESULT 11  
AAR74411  
ID AAR74411 standard; peptide: 35 AA.  
XX  
AC AAR74411;  
XX  
DT 01-DEC-1995 (first entry)  
XX  
DE Parathyroid hormone peptide analogue, Gly12,16,28,33.  
XX  
KW Analogue; truncated human parathyroid hormone; PTH; hPTH; substitution;  
KW osteoporosis; hypercalcaemia; hyperparathyroidism;

WO9511988-A.  
04-MAY-1995.  
25-OCT-1994, 94WO-US12205.  
25-OCT-1993; 93US-0142551.  
(AFFY-) AFFYMAX TECHNOLOGIES NV.  
Oldenburg KR, Selick HE;  
WPI: 1995-178880/23.  
New active analogues of parathyroid hormone - with increased  
activity, stability in serum etc., esp. for treating  
osteoporosis, also related DNA and vectors  
Claim 3; Page 86; 109pp; English.

XX The sequences given in AAR74411-26 represent analogues of the 34 amino  
CC acid sequence of truncated human parathyroid hormone (PTH). These  
CC analogues have increased activity and longer serum half life than  
CC native PTH due to eg. substitution of Met residues with Leu residues and  
CC replacing the carboxy Phe with Tyr. The carboxy terminal may also be  
CC modified by the addition of a homoserine residue or analogue, or by the  
CC addition of residues 35-84 of wild type PTH (see AAR74410). These PTH  
CC analogues may be used in the treatment of osteoporosis or  
CC hypercalcaemia, hyperparathyroidism or other metabolic bone diseases in  
CC human or veterinary medicine. These peptides may also have increased  
CC iontophoretic transdermal transport compared to wild type PTH and  
CC can be produced in high yield in recombinant E.coli.

SQ Sequence 35 AA;

Query Match 50.0%; Score 5; DB 16; Length 35;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGEH 5  
Db 10 NLGEH 14

RESULT 12  
AAR74396  
ID AAR74396 standard; peptide: 35 AA.  
XX  
AC AAR74396;  
XX  
DT 30-NOV-1995 (first entry)  
XX  
DE Parathyroid hormone peptide analogue, Glu13.  
XX  
KW Analogue; truncated human parathyroid hormone; PTH; hPTH; substitution;  
KW osteoporosis; hypercalcaemia; hyperparathyroidism;  
KW metabolic bone disease; human; veterinary medicine;  
KW iontophoretic transdermal transport; recombinant E.coli.

XX Synthetic.  
XX  
XX Key Location/Qualifiers

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FT Modified-site 35  
 FT /label= -H. OTHER  
 FT /note= "Homoserine (Hse), Hse lactone, Hse amide or  
 FT residues 35-84 of PTH"  
 PN WO9511988-A.  
 XX  
 XX  
 PD 04-MAY-1995.  
 XX  
 XX 25-OCT-1994; 94WO-US12205.  
 XX  
 XX 25-OCT-1993; 93US-0142551.  
 XX  
 XX (AFFY-) AFFYMAX TECHNOLOGIES NV.  
 XX  
 XX Oldenburg KR, Selick HE;  
 DR WPI; 1995-178880/23.  
 XX  
 XX New active analogues of parathyroid hormone - with increased  
 PT activity, stability in serum etc., esp. for treating  
 PT osteoporosis, also related DNA and vectors  
 XX  
 XX Claim 2: Page 85; 109pp; English.  
 XX  
 XX The sequences given in AAR74394-409 represent analogues of the 34 amino  
 CC acid sequence of truncated human parathyroid hormone (PTH). These  
 CC analogues have increased activity and longer serum half life than  
 CC native PTH due to substitution of Met residues with Leu residues and  
 CC replacing the carboxy Phe with Tyr. The carboxy terminal may also be  
 CC modified by the addition of a homoserine residue or analogue, or by the  
 CC addition of residues 35-84 of wild type PTH (see AAR74410). These PTH  
 CC analogues may be used in the treatment of osteoporosis or  
 CC hypercalcaemia, hyperparathyroidism or other metabolic bone diseases in  
 CC human or veterinary medicine. These peptides may also have increased  
 CC iontophoretic transdermal transport compared to wild type PTH and  
 CC can be produced in high yield in recombinant E.coli.  
 XX  
 XX Sequence 35 AA:  
 SQ  
 Query Match 50.0%; Score 5; DB 16; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 45;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 NLGEH 5  
 Db 10 NLGEH 14  
 |||||  
 RESULT 13  
 AAU63726  
 ID AAU63726 standard; Protein: 54 AA.  
 XX  
 XX AAU63726;  
 AC  
 XX 27-FEB-2002 (first entry)  
 DT  
 XX  
 XX Propionibacterium acnes immunogenic protein #24622.  
 DE  
 XX  
 XX SAPHO syndrome; synovitis; acne; pustulosis; hypertusis; osteomyelitis;  
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;  
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;  
 KW dermatological; osteopathic; neuroprotectant.  
 XX  
 XX Propionibacterium acnes.  
 OS  
 XX  
 XX WO200181581-A2.  
 PN  
 XX  
 XX 01-NOV-2001.  
 PD  
 XX 20-APR-2001; 2001WO-US12865.  
 PF  
 XX 21-APR-2000; 2000US-199047P.  
 PR

02-JUN-2000; 2000US-208841P.  
 07-JUL-2000; 2000US-216747P.  
 (CORI-) CORIXA CORP.  
 Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;  
 L'maisonneuve J, Zhang Y, Jen S, Carter D;  
 WPI: 2001-616774/71.  
 N-PSDB; AAS59634.  
 Propionibacterium acnes polypeptides and nucleic acids useful for  
 vaccinating against and diagnosing infections, especially useful for  
 treating acne vulgaris -  
 Example 1; SEQ ID No 24921; 1069pp; English.  
 Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic  
 polypeptides. The proteins and their associated DNA sequences are used in  
 the treatment, prevention and diagnosis of medical conditions caused by  
 P. acnes. The disorders include SAPHO syndrome (synovitis, acne,  
 pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.  
 P. acnes is also involved in infections of bone, joints and the central  
 nervous system, however it is particularly involved in the inflammatory  
 lesions associated with acne vulgaris. A method for detecting the  
 presence or absence of P. acnes in a patient comprises contacting a  
 sample with a binding agent that binds to the proteins of the invention  
 and determining the amount of bound protein in the sample. The  
 polypeptides may be used as antigens in the production of antibodies  
 specific for P. acnes proteins. These antibodies can be used to  
 downregulate expression and activity of P. acnes polypeptides and  
 therefore treat P. acnes infections. The antibodies may also be used as  
 diagnostic agents for determining P. acnes presence, for example, by  
 enzyme linked immunosorbent assay (ELISA).  
 Note: The sequence data for this patent did not form part of the printed  
 specification, but was obtained in electronic format directly from WIPO  
 at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 XX Sequence 54 AA:  
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 Query Match 50.0%; Score 5; DB 22; Length 54;  
 Best Local Similarity 100.0%; Pred. No. 64;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 HPVCD 9  
 Db 4 HPVCD 8  
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 XX  
 XX AAG14258;  
 AC  
 XX 17-OCT-2000 (first entry)  
 DT  
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 XX Arabidopsis thaliana protein fragment SEQ ID NO: 14050.  
 DE  
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 XX Protein identification; signal transduction pathway; metabolic pathway;  
 KW hybridisation assay; genetic mapping; gene expression control; promoter;  
 KW termination sequence.  
 XX  
 XX Arabidopsis thaliana.  
 OS  
 XX  
 XX EP1033405-A2.  
 PN  
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 XX 06-SEP-2000.  
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 XX 25-FEB-2000; 2000EP-0301439.  
 XX  
 XX 25-FEB-1999; 99US-0121825.  
 PF  
 XX 05-MAR-1999; 99US-0123180.  
 PR

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PR 01-APR-1999; 99US-0127462.  
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PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
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PR 21-APR-1999; 99US-0130449.  
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PR 28-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
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PR 14-MAY-1999; 99US-0134218.  
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PR 02-JUL-1999; 99US-0142055.  
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PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
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PR 22-JUL-1999; 99US-0145192.  
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PR 27-JUL-1999; 99US-0145913.  
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PR 28-JUL-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
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PR 06-AUG-1999; 99US-0147416.  
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PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
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PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.



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XX WPI; 2001-616774/71.  
DR N-PSDB; AAS59546.  
XX  
XX Propionibacterium acnes polypeptides and nucleic acids useful for  
PT vaccinating against and diagnosing infections, especially useful for  
PT treating acne vulgaris -  
XX  
XX Example 1: SEQ ID NO 11260; 1069pp; English.  
PS  
XX  
XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic  
CC polypeptides. The proteins and their associated DNA sequences are used in  
CC the treatment, prevention and diagnosis of medical conditions caused by  
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,  
CC pustulosis, hypertrophy and osteomyelitis), uveitis and the central  
CC P. acnes is also involved in infections of bone, joints and the inflammatory  
CC nervous system, however it is particularly involved in the inflammatory  
CC lesions associated with acne vulgaris. A method for detecting the  
CC presence or absence of P. acnes in a patient comprises contacting a  
CC sample with a binding agent that binds to the proteins of the invention  
CC and determining the amount of bound protein in the sample. The  
CC polypeptides may be used as antigens in the production of antibodies  
CC specific for P. acnes proteins. These antibodies can be used to  
CC downregulate expression and activity of P. acnes polypeptides and  
CC therefore treat P. acnes infections. The antibodies may also be used as  
CC diagnostic agents for determining P. acnes presence, for example, by  
CC enzyme linked immunosorbent assay (ELISA).  
CC Note: the sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 65 AA:

Query Match 50.0%; Score 5; DB 22; Length 65;  
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QY 3 GEHPV 7  
Db 3 GEHPV 7

Search completed: October 23, 2002, 12:19:35  
Job time : 32 secs

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PR 07-OCT-1999; 990S-0158029.  
PR 08-OCT-1999; 990S-0158232.  
PR 12-OCT-1999; 990S-0158369.  
PR 13-OCT-1999; 990S-0159293.  
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PR 13-OCT-1999; 990S-0159295.  
PR 14-OCT-1999; 990S-0159329.  
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PR 14-OCT-1999; 990S-0159638.  
PR 18-OCT-1999; 990S-0159584.  
PR 21-OCT-1999; 990S-0160741.  
PR 21-OCT-1999; 990S-0160767.  
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PR 21-OCT-1999; 990S-0160770.  
PR 21-OCT-1999; 990S-0160814.  
PR 21-OCT-1999; 990S-0160815.  
PR 22-OCT-1999; 990S-0160980.  
PR 22-OCT-1999; 990S-0160981.  
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PR 25-OCT-1999; 990S-0161404.  
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PR 25-OCT-1999; 990S-0161359.  
PR 26-OCT-1999; 990S-0161360.  
PR 26-OCT-1999; 990S-0161361.  
PR 28-OCT-1999; 990S-0161920.  
PR 28-OCT-1999; 990S-0161992.  
PR 28-OCT-1999; 990S-0161993.  
PR 28-OCT-1999; 990S-0161994.  
PR 29-OCT-1999; 990S-0162142.

Query Match 50.0%; Score 5; DB 21; Length 58;  
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QY 2 LGEHP 6  
Db 2 LGEHP 6

RESULT 15  
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XX AC AAU50065;  
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XX 27-FEB-2002 (first entry)  
XX  
XX Propionibacterium acnes immunogenic protein #10961.  
XX  
XX SAPHO syndrome; synovitis; acne; pustulosis; hypertrophy; osteomyelitis;  
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;  
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;  
KW dermatological; osteopathic; neuroprotectant.  
XX  
XX Propionibacterium acnes.  
XX  
XX WO200181581-A2.  
XX  
XX 01-NOV-2001.  
XX  
XX 20-APR-2001; 2001WO-US12865.  
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XX 21-APR-2000; 2000US-199047P.  
PR 02-JUN-2000; 2000US-208841P.  
PR 07-JUL-2000; 2000US-216747P.  
XX  
XX (CORI-) CORIXA CORP.  
PA  
XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;  
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;